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(54) Title: RECOMBINANT BONE MORPHOGENETIC PROTEIN HETERODIMERS, COMPOSITIONS AND METHODS OF USE (57) Abstract The present invention relates to methods for producing recombinant heterodimeric BMP proteins useful in the field of treating bone defects, healing bone injury and in wound healing in general. The invention also relates to the recombinant heterodimers and compositions containing them.		

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RECOMBINANT BONE MORPHOGENETIC PROTEIN HETERODIMERS,
COMPOSITIONS AND METHODS OF USE

Field of the Invention

5 The present invention relates to a series of
novel recombinant heterodimeric proteins useful in the
field of treating bone defects, healing bone injury and
in wound healing in general. The invention also relates
to methods for obtaining these heterodimers, methods for
10 producing them by recombinant genetic engineering
techniques, and compositions containing them.

Background of the Invention

 In recent years, protein factors which are
characterized by bone or cartilage growth inducing
15 properties have been isolated and identified. See, e.g.,
U. S. Patent No. 5,013,649, PCT published application
WO90/11366; PCT published application WO91/05802 and the
variety of references cited therein. See, also,
PCT/US90/05903 which discloses a protein sequence termed
20 OP-1, which is substantially similar to human BMP-7, and
has been reported to have osteogenic activity.

 A family of individual bone morphogenetic
proteins (BMPs), termed BMP-2 through BMP-9 have been
isolated and identified. Incorporated by reference for
25 the purposes of providing disclosure of these proteins

and methods of producing them are co-owned, co-pending U. S. Patent Application SN 721,847 and the related applications recited in its preamble. Of particular interest, are the proteins termed BMP-2 and BMP-4, disclosed in the above-referenced application; BMP-7, disclosed in SN 438,919; BMP-5, disclosed in SN 370,547 and SN 356,033; and BMP-6, disclosed in SN 370,544 and SN 347,559; and BMP-8, disclosed in SN 525,357. Additional members of the BMP family include BMP-1, disclosed in SN 655,578; BMP-9, disclosed in SN 720,590; and BMP-3, disclosed in SN 179,197 and PCT publication 89/01464. These applications are incorporated herein by reference for disclosure of these BMPs.

There remains a need in the art for other proteins and compositions useful in the fields of bone and wound healing.

Summary of the Invention

In one aspect, the invention provides a method for producing a recombinant heterodimeric protein having bone stimulating activity comprising culturing a selected host cell containing a polynucleotide sequence encoding a first selected BMP or fragment thereof and a polynucleotide sequence encoding a second selected BMP or fragment thereof. The resulting co-expressed, biologically active heterodimer is isolated from the culture medium.

According to one embodiment of this invention,

the host cell may be co-transfected with one or more vectors containing coding sequences for one or more BMPs. Each BMP polynucleotide sequence may be present on the same vector or on individual vectors transfected into the cell. Alternatively, the BMPs or their fragments may be incorporated into a chromosome of the host cell. Additionally, a single transcription unit may encode single copy of two genes encoding a different BMP.

According to another embodiment of this invention, the selected host cell containing the two polypeptide encoding sequences is a hybrid cell line obtained by fusing two selected, stable host cells, each host cell transfected with, and capable of stably expressing, a polynucleotide sequence encoding a selected first or second BMP or fragment thereof.

In another aspect of the present invention, therefore, there are provided recombinant heterodimeric proteins comprising a protein or fragment of a first BMP in association with a protein or fragment of a second BMP. The heterodimer may be characterized by bone stimulating activity. The heterodimers may comprise a protein or fragment of BMP-2 associated with a protein or fragment of either BMP-5, BMP-6, BMP-7 or BMP-8; or a protein or fragment of BMP-4 associated with a protein or fragment of either BMP-5, BMP-6, BMP-7 or BMP-8. In further embodiments the heterodimers may comprise a protein or fragment of BMP-2 associated with a protein or

fragment of either BMP-1, BMP-3 or BMP-4. BMP-4 may also form a heterodimer in association with BMP-1, BMP-2 or a fragment thereof. Still further embodiments may comprise heterodimers involving combinations of BMP-5, BMP-6, BMP-7 and BMP-8. For example, the heterodimers may comprise BMP-5 associated with BMP-6, BMP-7 or BMP-8; BMP-6 associated with BMP-7 or BMP-8; or BMP-7 associated with BMP-8. These heterodimers may be produced by co-expressing each protein in a selected host cell and isolating the heterodimer from the culture medium.

As a further aspect of this invention a cell line is provided which comprises a first polynucleotide sequence encoding a first BMP or fragment thereof and a second polynucleotide sequence encoding a second BMP or fragment thereof, the sequences being under control of one or more suitable expression regulatory systems capable of co-expressing the BMPs as a heterodimer. The cell line may be transfected with one or more than one polynucleotide molecule. Alternatively, the cell line may be a hybrid cell line created by cell fusion as described above.

Another aspect of the invention is a polynucleotide molecule or plasmid vector comprising a polynucleotide sequence encoding a first selected BMP or fragment thereof and a polynucleotide sequence encoding a second selected BMP or fragment thereof. The sequences are under the control of at least one suitable regulatory

sequence capable of directing co-expression of each protein or fragment. The molecule may contain a single transcription unit containing a copy of both genes, or more than one transcription unit, each containing a copy of a single gene.

As still another aspect of this invention there is provided a method for producing a recombinant dimeric or heterodimeric protein having bone stimulating activity in a prokaryotic cell comprising culturing a selected host cell containing a polynucleotide sequence encoding a first selected BMP or fragment thereof; culturing a second selected host cell containing a polynucleotide sequence encoding a second selected BMP or fragment thereof; isolating monomeric forms of each BMP protein from the culture medium and co-assembling a monomer of the first protein with a monomer of the second protein. The first protein and the second protein may be the same or different BMPs. The resulting biologically active dimer or heterodimer is thereafter isolated from the mixture. Preferred cells are E. coli.

Thus, as further aspects of this invention recombinant BMP dimers or heterodimers produced in eukaryotic cells are provided, as well as suitable vectors or plasmids, and selected transformed cells useful in such a production method.

Other aspects and advantages of the present invention are described further in the following detailed

description of preferred embodiments of the present invention.

Brief Description of the Figures

5 Figure 1 provides the DNA and amino acid sequences of human BMP-2 (SEQ ID NOS: 1 and 2).

Figure 2 provides the DNA and amino acid sequences of human BMP-4 (SEQ ID NOS: 3 and 4).

Figure 3 provides the DNA and amino acid sequences of human BMP-7 (SEQ ID NOS: 5 and 6).

10 Figure 4 provides the DNA and amino acid sequences of human BMP-6 (SEQ ID NOS: 7 and 8).

Figure 5 provides the DNA and amino acid sequences of human BMP-5 (SEQ ID NOS: 9 and 10).

15 Figure 6 provides the DNA and amino acid sequences of human BMP-8 (SEQ ID NOS: 11 and 12).

Figure 7 provides the DNA sequence of vector pALB2-781 containing the mature portoin of the BMP-2 gene (SEQ ID NOS: 13 and 14).

20 Figure 8 compares the activity of CHO BMP-2 and CHO BMP-2/7 in the W20 alkaline phosphatase assay.

Figure 9 compares the activity of CHO BMP-2 and CHO BMP-2/7 in the BGP (osteocalcin) assay.

25 Figure 10 provides a comparison of the W-20 activity of E. coli produced BMP-2 and BMP-2/7 heterodimer.

Figure 11 depicts BMP-3 DNA and amino acid sequence.

Figure 12 provides a comparison of BMP-2 and BMP-2/6

in the W-20 assay.

Figure 13 provides a comparison of the in vivo activity of BMP-2/6 and BMP-2.

Figure 14 provides a comparison of BMP-2, BMP-6 and
5 BMP-2/6 in vivo activity.

Detailed Description of the Invention

The present invention provides a method for producing recombinant heterodimeric proteins having bone stimulating activity, as well as the recombinant
10 heterodimers themselves, and compositions containing them for bone-stimulating or repairing therapeutic use.

As used throughout this document, the term 'heterodimer' is defined as a biologically-active protein construct comprising the association of two different BMP
15 protein monomers or active fragments thereof joined through at least one covalent, disulfide linkage. A heterodimer of this invention may be characterized by the presence of between one to seven disulfide linkages between the two BMP component strands.

20 According to the present invention, therefore, a method for producing a recombinant BMP heterodimer according to this invention comprises culturing a selected host cell containing a polynucleotide sequence encoding a first selected BMP or a biologically active
25 fragment thereof and a polynucleotide sequence encoding a second selected BMP or a fragment thereof. The resulting

co-expressed, biologically active heterodimer is formed within the host cell, secreted therefrom and isolated from the culture medium. Preferred embodiments of methods for producing the heterodimeric proteins of this invention, are described in detail below and in the following examples. Preferred methods of the invention involve known recombinant genetic engineering techniques [See, e.g., Sambrook et al, "Molecular Cloning. A Laboratory Manual:", 2d edition, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989)]. However, other methods, such as conventional chemical synthesis may also be useful in preparing a heterodimer of this invention.

BMP heterodimers generated by this method are produced in a mixture of homodimers and heterodimers. This mixture of heterodimers and homodimers may be separated from contaminants in the culture medium by resort to essentially conventional methods, such as classical protein biochemistry or affinity antibody columns specific for one of the BMPs making up the heterodimer. Additionally, if desired, the heterodimers may be separated from homodimers in the mixture. Such separation techniques allow unambiguous determination of the activity of the heterodimeric species. Example 4 provides one presently employed purification scheme for this purpose.

Preferably the recombinant heterodimers of this

invention produced by these methods involve the BMPs designated human BMP-2, human BMP-4, human BMP-5, human BMP-6, human BMP-7 and BMP-8. However, BMP-3 has also been determined to form an active heterodimer with BMP-2.

5 Other species of these BMPs as well as BMPs than those specifically identified above may also be employed in heterodimers useful for veterinary, diagnostic or research use. However, the human proteins, specifically those proteins identified below, are preferred for human
10 pharmaceutical uses.

Human BMP-2 is characterized by containing substantially the entire sequence, or fragments, of the amino acid sequence and DNA sequence disclosed in Figure 1. Human BMP-2 proteins are further characterized as
15 disulfide-linked dimers and homodimers of mature BMP-2 subunits. Recombinantly-expressed BMP-2 subunits include protein species having heterogeneous amino termini. One BMP-2 subunit is characterized by comprising amino acid #249 (Ser) - #396 (Arg) of Figure 1 (SEQ ID NOs: 1 and
20 2). Another BMP-2 subunit is characterized by comprising amino acid #266 (Thr) - #396 (Arg) of Figure 1. Another BMP-2 subunit is characterized by comprising amino acid #296 (Cys) - #396 (Arg) of Figure 1. A mature BMP-2 subunit is characterized by comprising amino acid #283
25 (Gln) - #396 (Arg) of Figure 1. This latter subunit is the presently most abundant protein species which results from recombinant expression of BMP-2 (Figure 1).

However, the proportions of certain species of BMP-2 produced may be altered by manipulating the culture conditions. BMP-2 may also include modifications of the sequences of Figure 1, e.g., deletion of amino acids #241-280 and changing amino acid #245 Arg to Ile, among other changes.

As described in detail in United States Patent Application SN 721,847, incorporated by reference herein, human BMP-2 may be produced by culturing a cell transformed with a DNA sequence comprising the nucleotide coding sequence from nucleotide #356 to #1543 in Figure 1 and recovering and purifying from the culture medium one or more of the above-identified protein species, substantially free from other proteinaceous materials with which it is co-produced. Human BMP-2 proteins are characterized by the ability to induce bone formation. Human BMP-2 also has in vitro activity in the W20 bioassay. Human BMP-2 is further characterized by the ability to induce cartilage formation. Human BMP-2 may be further characterized by the ability to demonstrate cartilage and/or bone formation activity in the rat bone formation assay described in the above-referenced application.

Human BMP-4 is characterized by containing substantially the entire sequence, or fragments, of the amino acid sequence and DNA sequence disclosed in Figure 2 (SEQ ID NOs: 3 and 4). Human BMP-4 proteins are

further characterized as disulfide-linked dimers and homodimers of mature BMP-4 subunits. Recombinantly-expressed BMP-4 subunits may include protein species having heterogeneous amino termini. A mature subunit of human BMP-4 is characterized by an amino acid sequence comprising amino acids #293 (Ser) - #408 (Arg) of Figure 2. Other amino termini of BMP-4 may be selected from the sequence of Figure 2. Modified versions of BMP-4, including proteins further truncated at the amino or carboxy termini, may also be constructed by resort to conventional mutagenic techniques.

As disclosed in above-incorporated patent application SN 721,847, BMP-4 may be produced by culturing a cell transformed with a DNA sequence comprising the nucleotide coding sequence from nucleotide #403 to nucleotide #1626 in Figure 2 and recovering and purifying from the culture medium a protein containing the amino acid sequence from amino acid #293 to #408 as shown in Figure 2, substantially free from other proteinaceous materials with which it is co-produced. BMP-4 proteins are capable of inducing the formation of bone. BMP-4 proteins are capable of inducing formation of cartilage. BMP-4 proteins are further characterized by the ability to demonstrate cartilage and/or bone formation activity in the rat bone formation assay.

Human BMP-7 is characterized by containing substantially the entire sequence, or fragments, of the

amino acid sequence and DNA sequence disclosed in Figure 3. Human BMP-7 proteins are further characterized as disulfide-linked dimers and homodimers of mature BMP-7 subunits. Recombinantly-expressed BMP-7 subunits include protein species having heterogeneous amino termini. One BMP-7 subunit is characterized by comprising amino acid #293 (Ser) - #431 (His) of Figure 3 (SEQ ID NOS: 5 and 6). This subunit is the most abundantly formed protein produced by recombinant expression of the BMP-7 sequence. Another BMP-7 subunit is characterized by comprising amino acids #300 (Ser) - #431 (His) of Figure 3. Still another BMP-7 subunit is characterized by comprising amino acids #316 (Ala) - #431 (His) of Figure 3. Other amino termini of BMP-7 may be selected from the sequence of Figure 3. Similarly, modified versions, including proteins further truncated at the amino or carboxy termini, of BMP-7 may also be constructed by resort to conventional mutagenic techniques.

As disclosed in above-incorporated patent application SN 438,919, BMP-7 may be produced by culturing a cell transformed with a DNA sequence comprising the nucleotide coding sequence from nucleotide #97 to nucleotide #1389 in Figure 3 and recovering and purifying from the culture medium a protein containing the amino acid sequence from amino acid #293 to #431 as shown in Figure 3, substantially free from other proteinaceous or contaminating materials with which it is

co-produced. These proteins are capable of stimulating, promoting, or otherwise inducing cartilage and/or bone formation.

Human BMP-6 is characterized by containing substantially the entire sequence, or fragments, of the amino acid sequence and DNA sequence disclosed in Figure 4. Human BMP-6 proteins are further characterized as disulfide-linked dimers of mature BMP-6 subunits. Recombinantly-expressed BMP-6 subunits may include protein species having heterogeneous amino termini. One BMP-6 subunit is characterized by comprising amino acid #375 (Ser) - #513 (His) of Figure 4 (SEQ ID NOs: 7 and 8). Other amino termini of BMP-6 may be selected from the sequence of Figure 4. Modified versions, including proteins further truncated at the amino or carboxy termini, of BMP-6 may also be constructed by resort to conventional mutagenic techniques.

As described in detail in United States Patent Application SN 490,033, incorporated by reference herein, human BMP-6 may be produced by culturing a cell transformed with a DNA sequence comprising the nucleotide coding sequence from nucleotide #160 to #1698 in Figure 4 and recovering and purifying from the culture medium a protein comprising amino acid #375 to #513 of Figure 4, substantially free from other proteinaceous materials or other contaminating materials with which it is co-produced. Human BMP-6 may be further characterized by

the ability to demonstrate cartilage and/or bone formation activity in the rat bone formation assay.

Human BMP-5 is characterized by containing substantially the entire sequence, or fragments, of the amino acid sequence and DNA sequence disclosed in Figure 5 (SEQ ID NOS: 9 and 10). Human BMP-5 proteins are further characterized as disulfide-linked dimers of mature BMP-5 subunits. Recombinantly-expressed BMP-5 subunits may include protein species having heterogeneous amino termini. One BMP-5 subunit is characterized by comprising amino acid #329 (Ser) - #454 (His) of Figure 5. Other amino termini of BMP-5 may be selected from the sequence of Figure 5. Modified versions, including proteins further truncated at the amino or carboxy termini, of BMP-5 may also be constructed by resort to conventional mutagenic techniques.

As described in detail in United States Patent Application SN 588,227, incorporated by reference herein, human BMP-5 may be produced by culturing a cell transformed with a DNA sequence comprising the nucleotide coding sequence from nucleotide #701 to #2060 in Figure 5 and recovering and purifying from the culture medium a protein comprising amino acid #329 to #454 of Figure 5, substantially free from other proteinaceous materials or other contaminating materials with which it is co-produced. Human BMP-5 may be further characterized by the ability to demonstrate cartilage and/or bone

formation activity in the rat bone formation assay described in the above-referenced application.

Human BMP-8 is characterized by containing substantially the entire sequence, or fragments, of the amino acid sequence and DNA sequence disclosed in Figure 6. Human BMP-8 proteins may be further characterized as disulfide-linked dimers of mature BMP-8 subunits. Recombinantly-expressed BMP-8 subunits may include protein species having heterogeneous amino termini. A BMP-8 sequence or subunit sequence comprises amino acid #143 (Ala) - #281 (His) of Figure 6 (SEQ ID NOS: 11 and 12). Other amino termini of BMP-8 may be selected from the sequence of Figure 6. Modified versions, including proteins further truncated at the amino or carboxy termini, of BMP-8 may also be constructed by resort to conventional mutagenic techniques.

As described generally in United States Patent Application SN 525,357, incorporated by reference herein, and as further described herein, human BMP-8 may be produced by culturing a cell transformed with a DNA sequence comprising the nucleotide coding sequence from nucleotide #1 to #850 in Figure 6 and recovering and purifying from the culture medium a protein comprising amino acid #143 to #281 of Figure 6, or similar amino acid sequences with heterogenous N-termini, substantially free from other proteinaceous materials or other contaminating materials with which it is co-produced.

This BMP-8 may also be produced in E. coli by inserting into a vector the sequence encoding amino acid #143 to 281 of Figure 6 with a Met inserted before amino acid #143. Human BMP-8 may be further characterized by the ability to demonstrate cartilage and/or bone formation activity in the rat bone formation assay.

Each above described BMP protein in its native, non-reduced dimeric form may be further characterized by an apparent molecular weight on a 12% Laemmli gel ranging between approximately 28kD to approximately 40kD. Analogs or modified versions of the DNA and amino acid sequences described herein which provide proteins or active fragments displaying bone stimulating or repairing activity in the rat bone formation assay described below in Example 9, are also classified as suitable BMPs for use in this invention, further provided that the proteins or fragments contain one or more Cys residues for participation in disulfide linkages. Useful modifications of these sequences may be made by one of skill in the art with resort to known recombinant genetic engineering techniques. Production of these BMP sequences in mammalian cells produces homodimers, generally mixtures of homodimers having heterologous N termini. Production of these BMP sequences in E.coli produces monomeric protein species.

Thus, according to this invention one recombinant heterodimer of the present invention

comprises the association of a human BMP-2, including, e.g., a monomeric strand from a mature BMP-2 subunit as described above or an active fragment thereof, bound through one or up to seven covalent, disulfide linkages to a human BMP-5 including, e.g., a monomeric strand from a mature BMP-5 subunit as described above or an active fragment thereof. Another recombinant heterodimer of the present invention comprises the association of a human BMP-2, as described above, bound through one or up to seven covalent, disulfide linkages to a human BMP-6, including, e.g., a monomeric strand from a BMP-6 subunit as described above or an active fragment thereof. Another recombinant heterodimer of the present invention comprises the association of a human BMP-2, as described above, bound through one or up to seven covalent, disulfide linkages to a human BMP-7, including, e.g., a monomeric strand of a BMP-7 subunit as described above or an active fragment thereof. Another recombinant heterodimer of the present invention comprises the association of a human BMP-2, as described above, bound through one or up to seven covalent, disulfide linkages to a human BMP-8, including, e.g., a monomeric strand of a BMP-8 subunit as described above or an active fragment thereof.

Still another recombinant heterodimer of the present invention comprises the association of a human BMP-4, including, e.g., a monomeric strand of a BMP-4

subunit as described above or an active fragment thereof,
bound through one or up to seven covalent, disulfide
linkages to a human BMP-5, as described above. Another
recombinant heterodimer of the present invention
5 comprises the association of a human BMP-4, as described
above, bound through one or more covalent, disulfide
linkages to a human BMP-6, as described above. Another
recombinant heterodimer of the present invention
comprises the association of a human BMP-4, as described
10 above bound through one or more covalent, disulfide
linkages to a human BMP-7, as described above. Another
recombinant heterodimer of the present invention
comprises the association of a human BMP-4, as described
above, bound through one or more covalent, disulfide
15 linkages to a human BMP-8, as described above.

A further recombinant heterodimer of the
present invention comprises the association of a human
BMP-2, including, e.g., a monomeric strand from a mature
BMP-2 subunit as described above or an active fragment
20 thereof, bound through at least one disulfide linkage to
a human BMP-3 including, e.g., a monomeric strand from a
mature BMP-3 subunit as described above or an active
fragment thereof. Another recombinant heterodimer of the
present invention comprises the association of a human
25 BMP-2, as described above, bound through at least one
disulfide linkage to a human BMP-4, including, e.g., a
monomeric strand from a BMP-4 subunit as described above.

or an active fragment thereof. Another recombinant heterodimer of the present invention comprises the association of a human BMP-5, as described above, bound through at least one disulfide linkage to a human BMP-6, including, e.g., a monomeric strand of a BMP-6 subunit as described above or an active fragment thereof. Another recombinant heterodimer of the present invention comprises the association of a human BMP-5, as described above, bound through at least one disulfide linkage to a human BMP-7, including, e.g., a monomeric strand of a BMP-7 subunit as described above or an active fragment thereof. In addition, human BMP-5 may be associated with human BMP-8 bound through at least one disulfide linkage to a human BMP-8 subunit or active fragment thereof.

Still another recombinant heterodimer of the present invention comprises the association of a human BMP-6, including, e.g., a monomeric strand of a BMP-6 subunit as described above or an active fragment thereof, bound through at least one disulfide linkage to a human BMP-7, as described above. Another recombinant heterodimer of the present invention comprises the association of a human BMP-6, as described above, bound through one or more covalent, disulfide linkages to a human BMP-8, as described above. Another recombinant heterodimer of the present invention comprises the association of a human BMP-7, as described above bound through one or more covalent, disulfide linkages to a

human BMP-8, as described above.

The disulfide linkages formed between the monomeric strands of the BMPs may occur between one Cys on each strand. Disulfide linkages may form between two Cys on each BMP. Disulfide linkages may form between three Cys on each BMP. Disulfide linkages may form between four Cys on each BMP. Disulfide linkages may form between five Cys on each BMP. Disulfide linkages may form between six Cys on each BMP. Disulfide linkages may form between seven Cys on each BMP. These disulfide linkages may form between adjacent Cys on each BMP or between only selected Cys interspersed within the respective protein sequence. Various heterodimers having the same BMP component strands may form with different numbers of disulfide linkages. Various heterodimers having the same BMP component strands may form with disulfide bonds at different Cys locations. Different heterodimers encompassed by this invention having the same BMP components may differ based upon their recombinant production in mammalian cells, bacterial cells, insect or yeast cells.

These recombinant heterodimers may be characterized by increased alkaline phosphatase activity in the W20 mouse stromal cell line bioassay (Example 8) compared to the individual BMP homodimers, one strand of which forms each heterodimer. Further, these heterodimers are characterized by greater activity in the

W20 bioassay than is provided by simple mixtures of the individual BMP dimers. Preliminary characterization of heterodimers measured on the W20 bioassay have demonstrated that heterodimers of BMP-2 with BMP-5, BMP-6 or BMP-7 are very active. Similarly, heterodimers of BMP-4 with BMP-5, BMP-6 or BMP-7 are strongly active in the W20 bioassay.

Heterodimers of this invention may also be characterized by activity in bone growth and stimulation assays. For example, a heterodimer of this invention is also active in the rat bone formation assay described below in Example 9. The heterodimers are also active in the osteocalcin bioassay described in Example 8. Other characteristics of a heterodimer of this invention include co-precipitation with anti-BMP antibodies to the two different constituent BMPs, as well as characteristic results on Western blots, high pressure liquid chromatography (HPLC) and on two-dimensional gels, with and without reducing conditions.

One embodiment of the method of the present invention for producing recombinant BMP heterodimers involves culturing a suitable cell line, which has been co-transfected with a DNA sequence coding for expression of a first BMP or fragment thereof and a DNA sequence coding for expression of a second BMP or fragment thereof, under the control of known regulatory sequences. The transformed host cells are cultured and the

heterodimeric protein recovered and purified from the culture medium.

In another embodiment of this method which is the presently preferred method of expression of the heterodimers of this invention, a single host cell, e.g., a CHO DUKX cell, is co-transfected with a first DNA molecule containing a DNA sequence encoding one BMP and a second DNA molecule containing a DNA sequence encoding a second selected BMP. One or both plasmids contain a selectable marker that can be used to establish stable cell lines expressing the BMPs. These separate plasmids containing distinct BMP genes on separate transcription units are mixed and transfected into the CHO cells using conventional protocols. A ratio of plasmids that gives maximal expression of activity in the W20 assay, generally, 1:1, is determined.

For example, as described in detail in Example 3, equal ratios of a plasmid containing the first BMP and a dihydrofolate reductase (DHFR) marker gene and another plasmid containing a second BMP and a DHFR marker gene can be co-introduced into DHFR-deficient CHO cells, DUKX-BII, by calcium phosphate coprecipitation and transfection, electroporation, microinjection, protoplast fusion or lipofection. Individual DHFR expressing transformants are selected for growth in alpha media with dialyzed fetal calf serum by conventional means. DHFR+ cells containing increased gene copies can be selected

for propagation in increasing concentrations of methotrexate (MTX) (e.g. sequential steps in 0.02, 0.1, 0.5 and 2.0 μ M MTX) according to the procedures of Kaufman and Sharp, J. Mol. Biol., 159:601-629 (1982); and Kaufman et al, Mol. Cell Biol., 5:1750 (1983). Expression of the heterodimer or at least one BMP linked to DHFR should increase with increasing levels of MTX resistance. Cells that stably express either or both BMP/DHFR genes will survive. However at a high frequency, cell lines stably incorporate and express both plasmids that were present during the initial transfection. The conditioned medium is thereafter harvested and the heterodimer isolated by conventional methods and assayed for activity. This approach can be employed with DHFR-deficient cells.

As an alternative embodiment of this method, a DNA molecule containing one selected BMP gene may be transfected into a stable cell line which already expresses another selected BMP gene. For example as described in detail in Example 3 below, a stable CHO cell line expressing BMP-7 with the DHFR marker (designated 7MB9) [Genetics Institute, Inc] is transfected with a plasmid containing BMP-2 and a second selectable marker gene, e.g., neomycin resistance (Neo). After transfection, the cell is cultured and suitable cells selected by treatment with MTX and the antibiotic, G-418. Surviving cells are then screened for the expression of

the heterodimer. This expression system has the advantage of permitting a single step selection.

Alternative dual selection strategies using different cell lines or different markers can also be used. For example, the use of an adenosine deaminase (ADA) marker to amplify the second BMP gene in a stable CHO cell line expressing a different BMP with the DHFR marker may be preferable, since the level of expression can be increased using deoxycoformycin (DCF)-mediated gene amplification. (See the ADA containing plasmid described in Example 1). Alternatively, any BMP cell line made by first using this marker can then be the recipient of a second BMP expression vector containing a distinct marker and selected for dual resistance and BMP coexpression.

Still another embodiment of a method of expressing the heterodimers of this invention includes transfecting the host cell with a single DNA molecule encoding multiple genes for expression either on a single transcription unit or on separate transcription units. Multicistronic expression involves multiple polypeptides encoded within a single transcript, which can be efficiently translated from vectors utilizing a leader sequence, e.g., from the EMC virus, from poliovirus, or from other conventional sources of leader sequences. Two BMP genes and a selectable marker can be expressed within a single transcription unit. For example, vectors

containing the configuration BMPx-EMC-BMPy-DHFR or BMPx-EMC-BMPy-EMC-DHFR can be transfected into CHO cells and selected and amplified using the DHFR marker. A plasmid may be constructed which contains DNA sequences encoding
5 two different BMPs, one or more marker genes and a suitable leader or regulatory sequence on a single transcription unit.

Similarly, host cells may be transfected with a single plasmid which contains separate transcription
10 units for each BMP. A selectable marker, e.g., DHFR, can be contained on a another transcription unit, or alternatively as the second cistron on one or both of the BMP genes. These plasmids may be transfected into a selected host cell for expression of the heterodimer, and
15 the heterodimer isolated from the cells or culture medium as described above.

Another embodiment of this expression method involves cell fusion. Two stable cell lines which express selected BMPs, such as a cell line expressing
20 BMP-2 (e.g., 2EG5) and a cell line expressing BMP-7 (e.g., 7MB9), developed using the DHFR/MTX gene amplification system and expressing BMP at high levels, as described in Example 1 and in the above incorporated U.S. applications, can be transfected with one of several
25 dominant marker genes (e.g., neo', hygromycin', GPT). After sufficient time in coculture (approximately one day) one resultant cell line expressing one BMP and a

dominant marker can be fused with a cell line expressing a different BMP and preferably a different marker using a fusigenic reagent, such as polyethylene glycol, Sendai virus or other known agent.

5 The resulting cell hybrids expressing both dominant markers and DHFR can be selected using the appropriate culture conditions, and screened for coexpression of the BMPs or their fragments. The selected hybrid cell contains sequences encoding both
10 selected BMPs, and the heterodimer is formed in the cell and then secreted. The heterodimer is obtained from the conditioned medium and isolated and purified therefrom by conventional methods (see e.g., Example 4). The resulting heterodimer may be characterized by methods
15 described herein.

Cell lines generated from the approaches described above can be used to produce co-expressed, heterodimeric BMP polypeptides. The heterodimeric proteins are isolated from the cell medium in a form
20 substantially free from other proteins with which they are co-produced as well as from other contaminants found in the host cells by conventional purification techniques. The presently preferred method of production is co-transfection of different vectors into CHO cells
25 and methotrexate-mediated gene amplification. Stable cell lines may be used to generate conditioned media containing recombinant BMP that can be purified and

assayed for in vitro and in vivo activities. For example, the resulting heterodimer-producing cell lines obtained by any of the methods described herein may be screened for activity by the assays described in Examples 8 and 9, RNA expression, and protein expression by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE).

The above-described methods of co-expression of the heterodimers of this invention utilize suitable host cells or cell lines. Suitable cell preferably include mammalian cells, such as Chinese hamster ovary cells (CHO). The selection of suitable mammalian host cells and methods for transformation, culture, amplification, screening and product production and purification are known in the art. See, e.g., Gething and Sambrook, Nature, 293:620-625 (1981), or alternatively, Kaufman et al, Mol. Cell. Biol., 5(7):1750-1759 (1985) or Howley et al, U. S. Patent 4,419,446. Other suitable mammalian cell lines are the CV-1 cell line, BHK cell lines and the 293 cell line. The monkey COS-1 cell line is presently believed to be inefficient in BMP heterodimer production.

Many strains of yeast cells known to those skilled in the art may also be available as host cells for expression of the polypeptides of the present invention, e.g., Saccharomyces cerevisiae. Additionally, where desired, insect cells may be utilized as host cells in the method of the present invention. See, e.g.,

Miller et al, Genetic Engineering, 8:277-298 (Plenum Press 1986) and references cited therein.

Another method for producing a biologically active heterodimeric protein of this invention may be employed where the host cells are microbial, preferably bacterial cells, in particular E. coli. For example, the various strains of E. coli (e.g., HB101, MC1061) are well-known as host cells in the field of biotechnology. Various strains of B. subtilis, Pseudomonas, other bacilli and the like may also be employed in this method.

This method, which may be employed to produce monomers and dimers (both homodimers and heterodimers) is described in European Patent Application No. 433,225, incorporated herein by reference. Briefly, this process involves culturing a microbial host comprising a nucleotide sequence encoding the desired BMP protein linked in the proper reading frame to an expression control sequence which permits expression of the protein and recovering the monomeric, soluble protein. Where the protein is insoluble in the host cells, the water-insoluble protein fraction is isolated from the host cells and the protein is solubilized. After chromatographic purification, the solubilized protein is subjected to selected conditions to obtain the biologically active dimeric configuration of the protein. This process, which may be employed to produce the heterodimers of this invention, is described specifically

in Example 7, for the production of a BMP-2 homodimer.

Another aspect of the present invention provides DNA molecules or plasmid vectors for use in expression of these recombinant heterodimers. These plasmid vectors may be constructed by resort to known methods and available components known to those of skill in the art. In general, to generate a vector useful in the methods of this invention, the DNA encoding the desired BMP protein is transferred into one or more appropriate expression vectors suitable for the selected host cell.

It is presently contemplated that any expression vector suitable for efficient expression in mammalian cells may be employed to produce the recombinant heterodimers of this invention in mammalian host cells. Preferably the vectors contain the selected BMP DNA sequences described above and in the Figures, which encode selected BMP components of the heterodimer. Alternatively, vectors incorporating modified sequences as described in the above-referenced patent applications are also embodiments of the present invention and useful in the production of the vectors.

In addition to the specific vectors described in Example 1, one skilled in the art can construct mammalian expression vectors by employing the sequence of Figures 1-6 or other DNA sequences containing the coding sequences of Figures 1-6 (SEQ ID NOs: 1, 3, 5, 7, 9 and

11), or other modified sequences and known vectors, such as pCD [Okayama et al, Mol. Cell Biol., 2:161-170 (1982)] and pJL3, pJL4 [Gough et al, EMBO J., 4:645-653 (1985)]. The BMP DNA sequences can be modified by removing the non-coding nucleotides on the 5' and 3' ends of the coding region. The deleted non-coding nucleotides may or may not be replaced by other sequences known to be beneficial for expression. The transformation of these vectors into appropriate host cells as described above can produce desired heterodimers.

One skilled in the art could manipulate the sequences of Figures 1-6 by eliminating or replacing the mammalian regulatory sequences flanking the coding sequence with e.g., yeast or insect regulatory sequences, to create vectors for intracellular or extracellular expression by yeast or insect cells. [See, e.g., procedures described in published European Patent Application 155,476] for expression in insect cells; and procedures described in published PCT application WO86/00639 and European Patent Application EPA 123,289 for expression in yeast cells].

Similarly, bacterial sequences and preference codons may replace sequences in the described and exemplified mammalian vectors to create suitable expression systems for use in the production of BMP monomers in the method described above. For example, the coding sequences could be further manipulated (e.g.,

ligated to other known linkers or modified by deleting non-coding sequences therefrom or altering nucleotides therein by other known techniques). The modified BMP coding sequences could then be inserted into a known bacterial vector using procedures such as described in T. Taniguchi et al, Proc. Natl. Acad. Sci. USA, 77:5230-5233 (1980). The exemplary bacterial vector could then be transformed into bacterial host cells and BMP heterodimers expressed thereby. An exemplary vector for microbial, e.g., bacterial, expression is described below in Example 7.

Other vectors useful in the methods of this invention may contain multiple genes in a single transcription unit. For example, a proposed plasmid p7E2D contains the BMP-7 gene followed by the EMC leader sequence, followed by the BMP-2 gene, followed by the DHFR marker gene. Another example is plasmid p7E2ED which contains the BMP-7 gene, the EMC leader, the BMP-2 gene, another EMC leader sequence and the DHFR marker gene. Alternatively, the vector may contain more than one transcription unit. As one example, the plasmid p2ED7ED contains a transcription unit for BMP-2 and a separate transcription unit for BMP-7, i.e., BMP-2-EMC-DHFR and BMP-7-EMC-DHFR. Alternatively, each transcription unit on the plasmid may contain a different marker gene. For example, plasmid p2EN7ED contains BMP-2-EMC-Neo and BMP-7-EMC-DHFR.

Additionally the vectors also contain appropriate expression control sequences which are capable of directing the replication and expression of the BMP in the selected host cells. Useful regulatory sequences for such vectors are known to one of skill in the art and may be selected depending upon the selected host cells. Such selection is routine and does not form part of the present invention. Similarly, the vectors may contain one or more selection markers, such as the antibiotic resistance gene, Neo or selectable markers such as DHFR and ADA. The presently preferred marker gene is DHFR. These marker genes may also be selected by one of skill in the art.

Once they are expressed by one of the methods described above, the heterodimers of this invention may be identified and characterized by application of a variety of assays and procedures. A co-precipitation (immunoprecipitation) assay may be performed with antibodies to each of the BMPs forming the heterodimer. Generally antibodies for this use may be developed by conventional means, e.g., using the selected BMP, fragments thereof, or synthetic BMP peptides as antigen. Antibodies employed in assays are generally polyclonal antibodies made from individual BMP peptides or proteins injected into rabbits according to classical techniques. This assay is performed conventionally, and permits the identification of the heterodimer, which is precipitated

by antibodies to both BMP components of the heterodimer. In contrast, only one of the two antibodies causes precipitation of any homodimeric form which may be produced in the process of producing the heterodimer.

5 Another characterizing assay is a Western assay, employing a precipitating antibody, a probing antibody and a detecting antibody. This assay may also be performed conventionally, by using an antibody to one of the BMPs to precipitate the dimers, which are run on
10 reducing SDS-PAGE for Western analysis. An antibody to the second BMP is used to probe the precipitates on the Western gel for the heterodimer. A detecting antibody, such as a goat-antirabbit antibody labelled with horseradish peroxidase (HRP), is then applied, which will
15 reveal the presence of one of the component subunits of the heterodimer.

 Finally, the specific activity of the heterodimer may be quantitated as described in detail in Example 6. Briefly, the amount of each BMP is
20 quantitated using Western blot analysis or pulse labelling and SDS-PAGE analysis in samples of each BMP homodimer and the heterodimer. The W20 activity is also determined as described specifically in Example 8. The relative specific activities may be calculated by the
25 formula: $\text{W20 alkaline phosphatase activity/amount of BMP}$ on Western blot or by fluorography. As one example, this formula has been determined for the BMP-2/7 heterodimer,

demonstrating that the heterodimer has an estimated 5 to 50 fold higher specific activity than the BMP-2 homodimer.

The heterodimers of the present invention may have a variety of therapeutic and pharmaceutical uses, e.g., in compositions for wound healing, tissue repair, and in similar compositions which have been indicated for use of the individual BMPs. Increased potency of the heterodimers over the individual BMPs may permit lower dosages of the compositions in which they are contained to be administered to a patient in comparison to dosages of compositions containing only a single BMP. A heterodimeric protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage defects in humans and other animals. Such a preparation employing a heterodimeric protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A heterodimeric protein of this invention may be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an

environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. Heterodimeric polypeptides of the invention may also be useful in the treatment of osteoporosis. A variety of osteogenic, cartilage-inducing and bone inducing factors have been described. See, e.g., European Patent Applications 148,155 and 169,016 for discussions thereof.

The proteins of the invention may also be used in wound healing and related tissue repair. The types of wounds include, but are not limited to burns, incisions and ulcers. (See, e.g., PCT Publication W084/01106 incorporated by reference herein for discussion of wound healing and related tissue repair).

Additionally, the proteins of the invention may increase neuronal survival and therefore be useful in transplantation and treatment of conditions exhibiting a decrease in neuronal survival.

In view of the usefulness of the heterodimers, therefore, a further aspect of the invention is a therapeutic method and composition for repairing fractures and other conditions related to cartilage and/or bone defects or periodontal diseases. In addition, the invention comprises therapeutic methods and compositions for wound healing and tissue repair. Such compositions comprise a therapeutically effective amount of a heterodimeric protein of the invention in admixture

with a pharmaceutically acceptable vehicle, carrier or matrix. The preparation and formulation of such physiologically acceptable protein compositions, having due regard to pH, isotonicity, stability and the like, is within the skill of the art.

It is expected that the proteins of the invention may act in concert with other related proteins and growth factors. Therapeutic methods and compositions of the invention therefore comprise a therapeutic amount of a heterodimeric protein of the invention with a therapeutic amount of at least one of the other BMP proteins disclosed in co-owned and concurrently filed U. S. applications described above. Such combinations may comprise separate molecules of the BMP proteins or other heteromolecules of the present invention.

In further compositions, heterodimeric proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications due to the lack of species specificity in BMP proteins. Particularly domestic animals and thoroughbred horses, in addition to

humans, are desired patients for such treatment with heterodimeric proteins of the present invention.

The therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than the heterodimeric proteins of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the heterodimeric BMP composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the heterodimeric protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical

properties, cosmetic appearance and interface properties. The particular application of the heterodimeric BMP compositions will define the appropriate formulation. Potential matrices for the compositions may be

5 biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well defined, such as bone or dermal collagen. Further

10 matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxyapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the

15 above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle

20 shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to

25 utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the BMP compositions from dissociating from the matrix.

The dosage regimen of a heterodimeric protein-containing pharmaceutical composition will be determined by the attending physician considering various factors which modify the action of the heterodimeric proteins, e.g. amount of bone weight desired to be formed, the site of bone damage, the condition of the damaged bone, the size of a wound, type of damaged tissue, the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and the BMP proteins in the heterodimer and any additional BMP or other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

The following examples are illustrative of the present invention and do not limit its scope.

EXAMPLE 1 - BMP Vector Constructs and Cell Lines

A. BMP-2 Vectors

The mammalian expression vector pMT2 CXM is a derivative of p91023 (b) [Wong et al, Science, 228:810-815 (1985)] differing from the latter in that it

contains the ampicillin resistance gene (Amp) in place of the tetracycline resistance gene (Tet) and further contains a XhoI site for insertion of cDNA clones. The functional elements of pMT2 CXM have been described [R. J. Kaufman, Proc. Natl. Acad. Sci. USA, 82:689-693 (1985)] and include the adenovirus VA genes, the SV40 origin of replication including the 72 bp enhancer, the adenovirus major late promoter including a 5' splice site and the majority of the adenovirus tripartite leader sequence present on adenovirus late mRNAs, a 3' splice acceptor site, a DHFR insert, the SV40 early polyadenylation site (SV40), and pBR322 sequences needed for propagation in E. coli.

EcoRI digestion of pMT2-VWF, which has been deposited with the American Type Culture Collection (ATCC), Rockville, MD (USA) under accession number ATCC 67122, excises the cDNA insert present in pMT2-VWF, yielding pMT2 in linear form. Plasmid pMT2 can be ligated and used to transform E. coli HB 101 or DH-5 to ampicillin resistance. Plasmid pMT2 DNA can be prepared by conventional methods.

Plasmid pMT2 CXM is then constructed using loopout/in mutagenesis [Morinaga et al, Biotechnology, 84:636 (1984)]. This removes bases 1075 to 1145 relative to the HindIII site near the SV40 origin of replication and enhancer sequences of pMT2. In addition it inserts the following sequence:

5' PO₄-CATGGGCAGCTCGAG-3' (SEQ ID NO: 15)

at nucleotide 1145. This sequence contains the recognition site for the restriction endonuclease XhoI.

A derivative of pMT2 CXM, termed plasmid pMT23, contains recognition sites for the restriction endonucleases PstI, EcoRI, Sall and XhoI.

Full length BMP-2 cDNA (Fig. 1) (SEQ ID NO: 1) is released from the λGT10 vector by digestion with EcoRI and subcloned into pSP65 [Promega Biotec, Madison, Wisconsin; see, e.g., Melton et al, Nucl. Acids Res., 12:7035-7056 (1984)] in both orientations yielding pBMP-2 #39-3 or pBMP-2 #39-4.

The majority of the untranslated regions of the BMP-2 cDNA are removed in the following manner. The 5' sequences are removed between the Sall site in the adapter (present from the original cDNA cloning) and the Sall site 7 base pairs upstream of the initiator ATG by digestion of the pSP65 plasmid containing the BMP-2 cDNA with Sall and religation. The 3' untranslated region is removed using heteroduplex mutagenesis using the oligonucleotide

5' GAGGGTTGTGGGTGTCGCTAGTGAGTCGACTACAGCAAAATT 3'.

End Sall

(SEQ ID NO: 16)

The sequence contains the terminal 3' coding region of the BMP-2 cDNA, followed immediately by a recognition site for Sall. The sequence introduces a Sall site following the termination (TAG) codon.

The SalI fragment of this clone was subcloned into the expression vector pMT23, yielding the vector pMT23-BMP2 Δ UT. Restriction enzyme sites flank the BMP-2 coding region in the sequence PstI-EcoRI-SalI-BMP-2 cDNA-SalI-EcoRI-XhoI.

The expression plasmid pED4 [Kaufman et al, Nucl. Acids Res., 19:4485-4490 (1991)] was linearized by digestion with EcoRI and treated with calf intestinal phosphatase. The BMP-2 cDNA gene was excised from pMT23-BMP2 Δ UT by digestion with EcoRI and recovery of the 1.2 kb fragment by electrophoresis through a 1.0% low melt agarose gel. The linearized pED4 vector and the EcoRI BMP-2 fragment were ligated together, yielding the BMP-2 expression plasmid pBMP2 Δ -EMC.

Another vector pBMP-2 Δ -EN contains the same sequences contained within the vector pBMP2 Δ -EMC, except the DHFR gene has been replaced by conventional means with the neomycin resistance gene from the Tn5 transposable element.

B. BMP4 Vectors

A BMP-4 cDNA sequence set forth in Figure 2 (SEQ ID NO: 3), in which the 3' untranslated region is removed, is made via heteroduplex mutagenesis with the mutagenic oligonucleotide:

5' GGATGTGGGTGCCGCTGACTCTAGAGTCGACGGAATTC 3'
End EcoRI
(SEQ ID NO: 17)

This deletes all of the sequences 3' to the translation
5 terminator codon of the BMP-4 cDNA, juxtaposing this
terminator codon and the vector polylinker sequences.
This step is performed in an SP65 vector [Promega
Biotech] and may also be conveniently performed in pMT2-
derivatives containing the BMP-4 cDNA similar to the BMP2
10 vectors described above. The 5' untranslated region is
removed using the restriction endonuclease BsmI, which
cleaves within the eighth codon of BMP-4 cDNA.

Reconstruction of the first eight codons
is accomplished by ligation to oligonucleotides:

15 EcoRI Initiator BsmI
5' AATTCACCATGATTCCTGGTAACCGAATGCT 3' (SEQ ID NO: 18)

and

3' GTGGTACTAAGGACCATTTGGCTTAC 5' (SEQ ID NO: 19)

These oligonucleotides form a duplex which has a BsmI
20 complementary cohesive end capable of ligation to the
BsmI restricted BMP-4 cDNA, and it has an EcoRI
complementary cohesive end capable of ligation to the
EcoRI restricted vector pMT2. Thus the cDNA for BMP-4
with the 5' and 3' untranslated regions deleted, and
25 retaining the entire encoding sequence is contained
within an EcoRI restriction fragment of approximately 1.2
kb.

The pMT2 CXM plasmid containing this BMP-4

sequence is designated pXMBMP-4 Δ UT. It is digested with EcoRI in order to release the BMP-4 cDNA containing insert from the vector. This insert is subcloned into the EcoRI site of the mammalian expression vector pED4, resulting pBMP4 Δ -EMC.

C. BMP-5 Vectors

A BMP-5 cDNA sequence comprising the nucleotide sequence from nucleotide #699 to #2070 of Fig. 5 (SEQ ID NO: 9) is specifically amplified as follows.

The oligonucleotides CGACCTGCAGCCACCATGCATCTGACTGTA (SEQ ID NO: 20) and TGCCTGCAGTTTAATATTAGTGGCAGC (SEQ ID NO: 21) are utilized as primers to allow the amplification of nucleotide sequence #699 to #2070 of Fig. 5 from the BMP-5 insert of λ -ZAP clone U2-16 [ATCC #68109]. This

procedure introduces the nucleotide sequence CGACCTGCAGCCACC (SEQ ID NO: 22) immediately preceding nucleotide #699 and the nucleotide sequence CTGCAGGCA immediately following nucleotide #2070. The addition of these sequences results in the creation of PstI

restriction endonuclease recognition sites at both ends of the amplified DNA fragment. The resulting amplified DNA product of this procedure is digested with the restriction endonuclease PstI and subcloned into the PstI site of the pMT2 derivative pMT21 [Kaufman, Nucl. Acids Res., 19:4485-4490 (1991)]. The resulting clone is designated H5/5/pMT.

The insert of H5/5/pMT is excised by PstI

digestion and subcloned into the plasmid vector pSP65 [Promega Biotech] at the PstI site, resulting in plasmid BMP5/SP6. BMP5/SP6 and U2-16 are digested with the restriction endonucleases NsiI and NdeI to excise the portion of their inserts corresponding to nucleotides #704 to #1876 of Fig. 5. The resulting 1173 nucleotide NsiI-NdeI fragment of clone U2-16 is ligated into the NsiI-NdeI site of BMP5/SP6 from which the corresponding 1173 nucleotide NsiI-NdeI fragment had been removed. The resulting clone is designated BMP5mix/SP65.

Direct DNA sequence analysis of BMP5mix/SP65 is performed to confirm identity of the nucleotide sequences produced by the amplification to those set forth in Fig. 5. The clone BMP5mix/SP65 is digested with the restriction endonuclease PstI resulting in the excision of an insert comprising the nucleotides #699 to #2070 of Fig. 5 and the additional sequences containing the PstI recognition sites as described above. The resulting 1382 nucleotide PstI fragment is subcloned into the PstI site of the pMT2 derivative pMT21. This clone is designated BMP5mix/pMT21#2.

The same fragment is also subcloned into the PstI site of pED4 to yield the vector designated BMP5mix-EMC-11.

D. BMP-6 Vectors

A BMP-6 cDNA sequence comprising the nucleotide sequence from nucleotide #160 to #1706 of

Fig. 4 (SEQ ID NO: 7) is produced by a series of techniques known to those skilled in the art. The clone BMP6C35 [ATCC 68245] is digested with the restriction endonucleases ApaI and TaqI, resulting in the excision of a 1476 nucleotide portion of the insert comprising nucleotide #231 to #1703 of Fig. 4. Synthetic oligonucleotides with SalI restriction endonuclease site converters are designed to replace those nucleotides corresponding to #160 to #230 and #1704 to #1706 which are not contained in the 1476 ApaI-TaqI fragment of the BMP-6 cDNA sequence.

Oligonucleotide/SalI converters conceived to replace the missing 5'

(TCGACCCACCATGCCGGGGCTGGGGCGGAGGGCGCAGTGGCTGT
GCTGGTGGTGGGGGCTGTGCTGCAGCTGCTGCGGGCC (SEQ ID NO: 23) and
CGCAGCAGCTGCACAGCAGCCCCCACCACCAGCACAGCCACTGCGCCCTCCGCCCCA
GCCCCGGCATGGTGGG) (SEQ ID NO: 24) and 3' (TCGACTGGTTT
(SEQ ID NO: 25) and CGAAACCAG (SEQ ID NO: 26)) sequences
are annealed to each other independently. The annealed
5' and 3' converters are then ligated to the 1476
nucleotide ApaI-TaqI described above, creating a 1563
nucleotide fragment comprising the nucleotide sequence
from #160 to #1706 of Fig. 4 and the additional sequences
contrived to create SalI restriction endonuclease sites
at both ends. The resulting 1563 nucleotide fragment is
subcloned into the SalI site of pSP64 [Promega Biotech,
Madison, WI]. This clone is designated BMP6/SP64#15.

DNA sequence analysis of BMP6/SP64#15 is performed to confirm identity of the 5' and 3' sequences replaced by the converters to the sequence set forth in Fig. 4. The insert of BMP6/SP64#15 is excised by digestion with the restriction endonuclease SalI. The resulting 1563 nucleotide SalI fragment is subcloned into the XhoI restriction endonuclease site of pMT21 and designated herein as BMP6/pMT21.

The PstI site of pED4 is converted to a SalI site by digestion of the plasmid with PstI and ligation to the converter oligonucleotides:

5'-TCGACAGGCTCGCCTGCA-3' (SEQ ID NO: 27) and

3'-GTCCGAGCGG-5' (SEQ ID NO: 28).

The above 1563 nucleotide SalI fragment is also subcloned into the SalI site of this pED4 vector, yielding the expression vector BMP6/EMC.

E. BMP-7 Vectors

A BMP-7 sequence comprising the nucleotide sequence from nucleotide #97 to #1402 of Fig. 3 (SEQ ID NO: 5) is specifically amplified as follows. The oligonucleotides CAGGTCGACCCACCATGCACGTGCGCTCA (SEQ ID NO: 29) and TCTGTCGACCTCGGAGGAGCTAGTGGC (SEQ ID NO: 30) are utilized as primers to allow the amplification of nucleotide sequence #97 to #1402 of Fig. 3 from the insert of clone PEH7-9 [ATCC #68182]. This procedure generates the insertion of the nucleotide sequence CAGGTCGACCCACC immediately preceeding nucleotide #97 and

the insertion of the nucleotide sequence GTCGACAGA immediately following nucleotide #1402. The addition of these sequences results in the creation of a SalI restriction endonuclease recognition site at each end of the amplified DNA fragment. The resulting amplified DNA product of this procedure is digested with the restriction endonuclease SalI and subcloned into the SalI site of the plasmid vector pSP64 [Promega Biotech, Madison, WI] resulting in BMP7/SP6#2.

The clones BMP7/SP6#2 and PEH7-9 are digested with the restriction endonucleases NcoI and StuI to excise the portion of their inserts corresponding to nucleotides #363 to #1081 of Fig. 3. The resulting 719 nucleotide NcoI-StuI fragment of clone PEH7-9 is ligated into the NcoI-StuI site of BMP7/SP6#2 from which the corresponding 719 nucleotide fragment is removed. The resulting clone is designated BMP7mix/SP6.

Direct DNA sequence analysis of BMP7mix/SP6 confirmed identity of the 3' region to the nucleotide sequence from #1082 to #1402 of Fig. 3, however the 5' region contained one nucleotide misincorporation.

Amplification of the nucleotide sequence (#97 to #1402 of Fig. 3) utilizing PEH7-9 as a template is repeated as described above. The resulting amplified DNA product of this procedure is digested with the restriction endonucleases SalI and PstI. This digestion results in the excision of a 747 nucleotide fragment

comprising nucleotide #97 to #833 of Fig. 3 plus the additional sequences of the 5' priming oligonucleotide used to create the SalI restriction endonuclease recognition site described earlier. This 747 SalI-PstI fragment is subcloned into a SalI-PstI digested pSP65 [Promega Biotech, Madison, WI] vector resulting in 5'BMP7/SP65. DNA sequence analysis demonstrates that the insert of the 5'BMP7/SP65#1 comprises a sequence identical to nucleotide #97 to #362 of Fig. 3.

10 The clones BMP7mix/SP6 and 5'BMP7/SP65 are digested with the restriction endonucleases SalI and NcoI. The resulting 3' NcoI-SalI fragment of BMP7mix/SP6 comprising nucleotides #363 to #1402 of Fig. 3 and 5' SalI-NcoI fragment of 5'BMP7/SP65 comprising nucleotides 15 #97 to #362 of Fig. 3 are ligated together at the NcoI restriction sites to produce a 1317 nucleotide fragment comprising nucleotides #97 to #1402 of Fig. 3 plus the additional sequences derived from the 5' and 3' oligonucleotide primers which allows the creation of SalI 20 restriction sites at both ends of this fragment.

 This 1317 nucleotide SalI fragment is ligated into the SalI site of the pMT2 derivative pMT2Cla-2. pMT2Cla-2 is constructed by digesting pMT21 with EcoRV and XhoI, treating the digested DNA with Klenow 25 fragment of DNA polymerase I and ligating ClaI linkers (NEBio Labs, CATCGATG). This removes bases 2171 to 2420 starting from the HindIII site near the SV40 origin of

replication and enhancer sequences of pMT2 and introduces a unique ClaI site, but leaves the adenovirus VAI gene intact, resulting in pMT2Cla-2. This clone is designated BMP-7-pMT2.

5 The insert of BMP-7-pMT2 is excised by digestion with the restriction endonuclease SalI. The resulting 1317 nucleotide SalI fragment is subcloned into the XhoI restriction endonuclease site of pMT21 to yield the clone BMP-7/pMT21. This SalI fragment is also
10 subcloned into the SalI site of the pED4 vector in which the PstI site was converted into a SalI site as described above, resulting in the vector pBMP7/EMC#4.

F. BMP-8 Vectors

 At present no mammalian BMP-8 vectors have
15 been constructed. However, using the sequence of Figure 6 (SEQ ID NO: 11), it is contemplated that vectors similar to those described above for the other BMPs may be readily constructed. A bacterial expression vector similar to the BMP-2 vector described in detail in
20 Example 7 may also be constructed for BMP-8, by introducing a Met before the amino acid #284 Ala of Fig. 6. This sequence of BMP-8 is inserted into the vector pALBP2-781 in place of the BMP-2 sequence. See Example
25 7.

G. BMP Vectors Containing the Adenosine Deaminase (Ada) Marker

BMP genes were inserted into the vector

pMT3SV2Ada [R. J. Kaufman, Meth. Enz., 185:537-566 (1990)] to yield expression plasmids containing separate transcription units for the BMP cDNA gene and the selectable marker Ada. pMT3SV2Ada contains a polylinker with recognition sites for the enzymes PstI, EcoRI, SalI and XbaI that can be used for insertion of and expression of genes (i.e. BMP) in mammalian cells. In addition, the vector contains a second transcription unit encoding Ada which serves as a dominant and amplifiable marker in mammalian cells.

To construct expression vectors for BMP-5, BMP-6 and BMP-7, individually, the same general method was employed. The gene for BMP 5 (Fig. 5), 6 (Fig. 4) or 7 (Fig. 3) was inserted into the polylinker essentially as described above for the pED4 vector. These vectors can be used for transfection into CHO DUKX cells and subsequent selection and amplification using the Ada marker as previously described [Kaufman et al, Proc. Natl. Acad. Sci. USA, 83:3136-3140 (1986)]. Since each such vector does not contain a DHFR gene, the resultant transformed cells remain DHFR negative and can be subsequently transfected with a second vector containing a different BMP in conjunction with DHFR and amplified with methotrexate.

Alternatively, the pMT3SV2Ada/BMP vectors can be used to transfect stable CHO cell lines previously transfected with a different BMP gene and amplified using

the DHFR/methotrexate system. The resultant transfectants can be subsequently amplified using the Ada system, yielding cell lines that coexpress two different BMP genes, and are amplified using both the DHFR and Ada markers.

H. BMP-Expressing Mammalian Cell Lines

At present, the most desirable mammalian cell lines for use in producing the recombinant homodimers and heterodimers of this invention are the following. These cell lines were prepared by conventional transformation of CHO cells using vectors described above.

The BMP-2 expressing cell line 2EG5 is a CHO cell stably transformed with the vector pBMP2delta-EMC.

The BMP-4 expressing cell line 4E9 is a CHO cell stably transformed with the vector pBMP4delta-EMC.

The BMP-5 expressing cell line 5E10 is a CHO cell stably transformed with the vector BMP5mix-EMC-11 (at a amplification level of 2 micromolar MTX).

The BMP-6 expressing cell line 6HG8 is a CHO cell stably transformed with the vector BMP6/EMC.

The BMP-7 expressing cell line 7MB9 is a CHO cell stably transformed with the vector BMP7/pMT21.

EXAMPLE 2 - TRANSIENT EXPRESSION OF BMP HETERODIMERS

The heterodimers of the present invention may be prepared by co-expression in a transient expression system for screening in the assays of Example 8 by two different techniques as follows.

5 In the first procedure, the pMT2-derived and EMC-derived expression plasmids described in Example 1 and other similarly derived vectors were constructed which encoded, individually, BMP-2 through BMP-7, and transforming growth factor-beta ($TGF\beta 1$). All
10 combinations of pairs of plasmids were mixed in equal proportion and used to co-transfect CHO cells using the DEAE-dextran procedure [Sompayrac and Danna, Proc. Natl. Acad. Sci. USA, 78:7575-7578 (1981); Luthman and Magnusson, Nucl. Acids Res., 11:1295-1308 (1983)]. The
15 cells are grown in alpha Minimal Essential Medium (α -MEM) supplemented with 10% fetal bovine serum, adenosine, deoxyadenosine, thymidine (100 μ g/ml each), pen/strep, and glutamine (1 mM).

 The addition of compounds such as heparin,
20 suramin and dextran sulfate are desirable in growth medium to increase the amounts of BMP-2 present in the conditioned medium of CHO cells. Similarly responsive to such compounds is BMP-5. Therefore, it is expected that these compounds will be added to growth medium for any
25 heterodimer containing these BMP components. Other BMPs may also be responsive to the effects of these compounds, which are believed to inhibit the interaction of the

mature BMP molecules with the cell surface.

The following day, fresh growth medium, with or without 100 μ g/ml heparin, was added. Twenty-four hours later, conditioned medium was harvested.

5 In some experiments, the conditioned medium was collected minus heparin for the 24-48 hour period post-transfection, and the same plates were then used to generate conditioned medium in the presence of heparin 48-72 hour post-transfection. Controls included
10 transfecting cells with expression plasmids lacking any BMP sequences, transfecting cells with plasmids containing sequences for only a single BMP, or mixing conditioned medium from cells transfected with a single BMP with conditioned medium from cells transfected with a
15 different BMP.

Characterizations of the coexpressed heterodimer BMPs in crude conditioned media, which is otherwise not purified, provided the following results. Transiently coexpressed BMP was assayed for induction of
20 alkaline phosphatase activity on W20 stromal cells, as described in Example 8.

Co-expression of BMP-2 with BMP-5, BMP-6 and BMP-7, and BMP-4 with BMP-5, BMP-6 and BMP-7 yielded more alkaline phosphatase inducing activity in the W20 assay
25 than either of the individual BMP homodimers alone or mixtures of homodimers, as shown below. Maximal activity (in vitro), was obtained when BMP-2 was coexpressed with

55

BMP-7. Increased activity was also found the heterodimers BMP-2/5; BMP-2/6; BMP-4/5; BMP-4/6; and BMP-4/7.

	Condition Medium						
	TGF- β	BMP-7	BMP-6	BMP-5	BMP-4	BMP-3	BMP-2
BMP-2	33	240	99	89	53	9	29
BMP-3	-	-	-	-	14	-	
BMP-4	12	115	25	22	24		
BMP-5	-	-	-	-			
BMP-6	-	-	-				
BMP-7	-	-					
TGF- β	-						

	Condition Medium + heparin						
	TGF- β	BMP-7	BMP-6	BMP-5	BMP-4	BMP-3	BMP-2
BMP-2	88	454	132	127	70	77	169
BMP-3	-	-	-	-	7	-	
BMP-4	7	119	30	41	37		
BMP-5	-	-	-	-			
BMP-6	-	-	-				
BMP-7	-	-					
TGF- β	-						

Units: 1 unit of activity is equivalent to that of 1 ng/ml of rhBMP-2.

-: indicates activity below the detection limit of the assay.

These BMP combinations were subsequently expressed using various ratios of expression plasmids (9:1, 3:1, 1:1, 1:3, 1:9) during the CHO cell transient transfection. The performance of this method using plasmids containing BMP-2 and plasmids containing BMP-7 at plasmid number ratios ranging from 9:1 to 1:9, respectively, demonstrated that the highest activity in

the W20 assay was obtained when approximately the same number of plasmids of each BMP were transfected into the host cell. Ratios of BMP-2 to BMP-7 plasmids of 3:1 to 1:3, respectively, also resulted in increased activity in
5 W20 assay in comparison to host cells transfected with plasmids containing only a single BMP. However, these latter ratios produced less activity than the 1:1 ratio.

Similar ratios may be determined by one of skill in the art for heterodimers consisting of other
10 than BMP-2 and BMP-7. For example, preliminary work on the heterodimer formed between BMP-2 and BMP-6 has indicated that a preferred ratio of plasmids for co-transfection is 3:1, respectively. The determination of preferred ratios for this method is within the skill of
15 the art.

As an alternative means to transiently generate coexpressed BMPs, the stable CHO cell lines identified in Example 1 expressing each BMP-2, BMP-4, BMP-5, BMP-6 and BMP-7, are cocultured for one day, and are then fused
20 with 46.7% polyethylene glycol (PEG). One day post-fusion, fresh medium is added and the heterodimers are harvested 24 hours later for the W20 assay, described in Example 8. The assay results were substantially similar to those described immediately above.

25 Therefore, all combinations of BMP-2 or 4 coexpressed with either BMP-5, 6 or 7 yielded greater activity than any of the BMP homodimers alone. In

control experiments where each BMP homodimer was expressed alone and conditioned media mixed post harvest, the activity was always intermediate between the individual BMPs, demonstrating that the BMP co-expressed heterodimers yield higher activity than combinations of the individually expressed BMP homodimers.

EXAMPLE 3 - STABLE EXPRESSION OF BMP HETERODIMERS

A. BMP-2/7

Based on the results of the transient assays in Example 2, stable cell lines were made that co-express BMP-2 and BMP-7.

A preferred stable cell line, 2E7E-10, was obtained as follows: Plasmid DNA (a 1:1 mixture of pBMP-7-EMC and pBMP-2-EMC, described in Example 1) is transfected into CHO cells by electroporation [Neuman et al, EMBO J., 1:841-845 (1982)].

Two days later, cells are switched to selective medium containing 10% dialyzed fetal bovine serum and lacking nucleosides. Colonies expressing DHFR are counted 10-14 days later. Individual colonies or pools of colonies are expanded and analyzed for expression of each heterodimer BMP component RNA and protein using standard procedures and are subsequently selected for amplification by growth in increasing concentrations of MTX. Stepwise selection of the preferred clone, termed 2E7E, is carried out up to a concentration of 0.5 μ M MTX.

The cell line is then subcloned and assayed for heterodimer 2/7 expression.

Procedures for such assay include Western blot analysis to detect the presence of the component DNA, protein analysis and SDS-PAGE analysis of metabolically labelled protein, W20 assay, and analysis for cartilage and/or bone formation activity using the ectopic rat bone formation assay of Example 9. The presently preferred clonally-derived cell line is identified as 2E7E-10. This cell line secretes BMP-2/7 heterodimer proteins into the media containing 0.5 μ M MTX.

The CHO cell line 2E7E-10 is grown in Dulbecco's modified Eagle's medium (DMEM)/Ham's nutrient mixture F-12, 1:1 (vol/vol), supplemented with 10% fetal bovine serum. When the cells are 80 to 100% confluent, the medium is replaced with serum-free DMEM/F-12. Medium is harvested every 24 hours for 4 days. For protein production and purification the cells are cultured serum-free.

While the co-expressing cell line 2E7E-10 preliminarily appears to make lower amounts of BMP protein than the BMP2-expressing cell line 2EG5 described in Example 2, preliminary evidence suggests that the specific activity of the presumptive heterodimer is at least 5-fold greater than BMP-2 homodimer (see Example 6).

To construct another heterodimer producing cell

line, the stable CHO cell line 7MB9, previously transfected with pBMP-7-pMT2, and which expresses BMP-7, is employed. 7MB9 may be amplified and selected to 2 μ M methotrexate resistance using the DHFR/MTX system. To generate a stable co-expressing cell line, cell line 7MB9 is transfected with the expression vector pBMP-2 Δ -EN (EMC-Neo) containing BMP-2 and the neomycin resistance gene from the Tn5 transposable element. The resulting transfected stable cell line was selected for both G-418 and MTX resistance. Individual clones were picked and analyzed for BMP expression, as described above.

It is anticipated that stable cell lines co-expressing other combinations of BMPs which show enhanced activity by transient coexpression will likewise yield greater activity upon stable expression.

B. BMP-2/6

Based on the results of the transient assays in Example 2, stable cell lines were made that co-express BMP-2 and BMP-6.

A preferred stable cell line, 12C07, was obtained as follows: Plasmid DNA (a 1:3 mixture of pBMP-6-EMC and pBMP-2-EMC, described in Example 1) is transfected into CHO cells by electroporation [Neuman et al, EMBO J., 1:841-845 (1982)].

Two days later, cells are switched to selective medium containing 10% dialyzed fetal bovine serum and lacking nucleosides. Colonies expressing DHFR are

counted 10-14 days later. Individual colonies or pools of colonies are expanded and analyzed for expression of each heterodimer BMP component RNA and protein using standard procedures and are subsequently selected for amplification by growth in increasing concentrations of MTX. Stepwise selection of the preferred clone, termed 12-C, is carried out up to a concentration of 2.0 μ M MTX. The cell line is then subcloned and assayed for heterodimer 2/6 expression.

Procedures for such assay include Western blot analysis to detect the presence of the component DNA, protein analysis and SDS-PAGE analysis of metabolically labelled protein, W20 assay, and analysis for cartilage and/or bone formation activity using the ectopic rat bone formation assay of Example 9. The presently preferred clonally-derived cell line is identified as 12C07. This cell line secretes BMP-2/6 heterodimer proteins into the media containing 2.0 μ M MTX.

The CHO cell line 12C07 is grown in Dulbecco's modified Eagle's medium (DMEM)/Ham's nutrient mixture F-12, 1:1 (vol/vol), supplemented with 10% fetal bovine serum. When the cells are 80 to 100% confluent, the medium is replaced with serum-free DMEM/F-12. Medium is harvested every 24 hours for 4 days. For protein production and purification the cells are cultured serum-free.

While the co-expressing cell line 12C07

preliminarily appears to make lower amounts of BMP protein than the BMP2-expressing cell line 2EG5 described in Example 2, preliminary evidence suggests that the specific activity of the presumptive heterodimer is at least 3-5-fold greater than BMP-2 homodimer (see Example 6).

To construct another heterodimer producing cell line, the stable CHO cell line 2EG5, previously transfected with pBMP-2-EMC, and which expresses BMP-2, is employed. 2EG5 may be amplified and selected to 2 μ M methotrexate resistance using the DHFR/MTX system. To generate a stable co-expressing cell line, cell line 2EG5 is transfected with the expression vector pBMP-6-ada (ada deaminase) containing BMP-6 and the ADA resistance gene. The resulting transfected stable cell line was selected for both DCF and MTX resistance. Individual clones are picked and analyzed for BMP expression, as described above.

It is anticipated that stable cell lines co-expressing other combinations of BMPs which show enhanced activity by transient coexpression will likewise yield greater activity upon stable expression.

EXAMPLE 4-PURIFICATION OF BMP2/7 AND BMP-2/6 HETERODIMER

The same purification procedure is used for BMP-2/6 heterodimer and BMP-2/7 heterodimer. Conditioned media from cultures of cell line 2E7E-10 or 12C07 containing

recombinantly produced BMP heterodimer 2/7V or 2/6, respectively, can be generated from either adherent or suspension cultures. For small to medium scale generation of coexpressed BMP, adherent cultures are seeded into roller bottles and allowed to grow to confluence in alpha-Minimal Eagles Medium [α -MEM, Gibco, Grand Island, NY] containing 10% dialyzed heat-inactivated fetal calf serum [Hazleton, Denver, PA]. The media is then switched to a serum-free, albumin free, low protein medium based on a 50:50 mixture of Delbecco's Modified Eagle's medium and Hams F-12 medium, optionally supplemented with 100 micrograms/ml dextran sulfate. Four or five daily harvests are pooled, and used to purify the recombinant protein.

Conditioned medium from roller bottle cultures obtained as described above was thawed slowly at room temperature and pooled. The pH of the pooled medium was adjusted to pH 8.0 using 1 M Tris, pH 8.0. A column was poured containing Matrex Cellufine Sulfate [Amicon] and equilibrated in 50 mM Tris, pH 8.0.

Upon completion of loading of the medium, the column was washed with buffer containing 50 mM Tris, 0.4 M NaCl, pH 8.0 until the absorbance at 280 nm reached baseline. The column was then washed with 50 mM Tris, pH 8.0 to remove NaCl from the buffer. The resin was then washed with 50 mM Tris, 0.2 M NaCl, 4 M Urea, pH 8.0 until a peak had eluted. The column was then washed into

50 mM Tris, pH 8.0 to remove the urea.

The bound BMP-2/7 or BMP-2/6 was then eluted using 50 mM Tris, 0.5 M NaCl, 0.5 M Arginine, pH 8.0.

The eluate was collected as a single pool and may be

5 optionally stored frozen prior to further purification.

This Cellufine Sulfate eluate was diluted with 14 volumes of 6M urea and the pH of the sample was then adjusted to

6.0. A hydroxyapatite-Ultrogel [IBF] column was poured and equilibrated with 80 mM potassium phosphate, 6M urea,
10 pH 6.0.

After the completion of sample loading, the column was washed with 10 bed volumes of the

equilibration buffer. Bound BMP-2/7 or BMP-2/6

heterodimers were eluted with 5 bed volumes of 100 mM

15 potassium phosphate, 6M urea, pH 7.4. This eluate was loaded directly onto a Vydac C₄ reverse-phase HPLC column equilibrated in water - 0.1% TFA. BMP-2/7 or BMP-2/6 heterodimers were eluted with a gradient of 30-50% acetonitrile in water - 0.1% trifluoroacetic acid.

20 Fractions containing BMPs are identified by SDS-PAGE in the presence or absence of reductant. The identity of the BMPs with respect to the heterodimers vs. homodimers is determined by 2D-PAGE (+/- reductant). Fractions with heterodimers gave bands which reduce to two spots. Bands
25 from homodimer fractions reduce to a single spot for each BMP species.

The BMP-2/6 heterodimer subunits are analyzed on a protein sequenator. BMP-2/6 heterodimers of the followig species are present: BMP-6 subunit beginning with amino acid #375 Ser-Ala-Ser-Ser in association with
5 BMP-2 subunit beginning with amino acid #283 Gin-Ala-Lys or #249 Ser-Lev-His, though other less abundant species may be present.

It is contemplated that the same or substantially similar purification techniques may be employed for any
10 recombinant BMP heterodimer of this invention. The hydroxyapatite-Ultrogel column may be unnecessary and that the purification scheme may be modified by loading the Cellufine Sulfate eluate directly onto the C₄ reverse-phase HPLC column without use of the former column for
15 BMP2/7 or BMP-2/6 or the other heterodimers of this invention.

EXAMPLE 5 - PROTEIN CHARACTERIZATION

Total protein secreted from the co-expressing cell lines is analyzed after labelling with ³⁵S-methionine
20 or by Western blot analysis using antibodies raised against both BMPs of the heterodimer, e.g., BMP-2 and BMP-7. Together with the alkaline phosphatase assays, the data indicates the presence of the heterodimer and the specific activity. The following specific details
25 are directed towards data collected for the BMP-2/7 and BMP-2/6 heterodimers; however, by application of similar

methods to the other heterodimers described herein,
similar results are expected.

A. ³⁵S-Met labelling

Cell lines derived by cotransfection of
5 BMP2 Δ -EMC and BMP7 Δ -EMC expression vectors were pulsed
with ³⁵S-methionine for 15 minutes, and chased for 6 hours
in serum free media in the presence or absence of
heparin. Total secreted protein was analyzed under
reducing conditions by PAGE and fluorography. The
10 results demonstrate that several cell lines secrete both
BMP-2 and BMP-7 protein. There is a good correlation
between the amount of alkaline phosphatase activity and
the amount of coexpressed protein.

Several cell lines secrete less total BMP-
15 2 and 7 than the BMP-2-only expressing cell line 2EG5,
which produces 10 μ g/ml BMP-2. Cell line 2E7E-10
(amplified at a level of 0.5mM MTX) secretes equal
proportions of BMP-2 and BMP-7 at about the same overall
level of expression as the cell line 2EG5. Cell line
20 2E7E-10 produces the equivalent of 600 micrograms/ml of
BMP-2 homodimer activity in one assay.

Total labelled protein was also analyzed on a
two-dimensional non-reducing/reducing gel system to
ascertain whether a heterodimer is made. Preliminary
25 results demonstrate the presence of a unique spot in this
gel system that is not found in either the BMP-2-only or
BMP-7-only cell lines, suggesting the presence of 2/7

heterodimer. The same gel with purified material produced the same results (e.g., two unique spots on the gel) indicative of the presence of the 2/7 heterodimer. The homodimer of BMP2 produced distinct species on this gel system.

In contrast to the recombinant BMP-2/7 purification, BMP-2 homodimers are not detected during the BMP-2/6 preparation; however, significant amounts of BMP-6 homodimers are found. In addition, a significant amount of a -20 amino acid N-terminal truncated form of BMP-6 is found; this could be eliminated by the inclusion of protease inhibitors during cell culture. BMP-2/6 was found to elute two to three fractions later from C4 RP-HPLC than did BMP-2/7.

Amino acid sequencing indicates that the predominant BMP-2/7 heterodimer species comprises a mature BMP-2 subunit [amino acid #283(Gln)-#396(Arg)] and a mature subunit of BMP-7 [#293(Ser)-#431(His)]. BMP-2/6 heterodimer comprises the mature BMP-2 subunit (#283-396) and the mature BMP-6 subunit [#375(Ser)-#513(His)].

B. Immunoprecipitation coupled to Western blot analysis

Conditioned media from a BMP-2-only (2EG5), a BMP-7-only (7MB9), or the 2E7E-10 co-expressing cell line were subjected to immunoprecipitation with either a BMP-2 or BMP-7 antibody (both conventional

polyclonal antibodies raised in rabbits), then analyzed on Western blots probed with either an anti-BMP-2 or anti-BMP-7 antibody. The 2/7 heterodimer precipitates and is reactive on Western blots with both the BMP-2 and BMP-7 antibodies, while either BMP by itself reacts with its specific antibody, but not with the reciprocal antibody.

It has been demonstrated using this strategy that a protein in the co-expressing cell line that is precipitated by the anti-BMP-7 antibody W33 [Genetics Institute, Inc, Cambridge, Massachusetts] and reacts on a Western blot with the anti-BMP-2 antibody W12 or W10 [Genetics Institute, Inc.] is not present in the BMP-2 or 7-only expressing cell lines. This experiment indicates that this protein species is the heterodimeric protein. Conversely, precipitation with W12 and probing with W33 yielded similar results.

EXAMPLE 6 - SPECIFIC ACTIVITY OF HETERODIMERS

A. In vitro Assays

The specific activity of the BMP-2/7 or BMP-2/6 heterodimer and the BMP-2 homodimer secreted into growth medium of the stable cell lines 2E7E-10 and 2EG55, and 12C07 and 2EG5, respectively, were estimated as follows.

The amount of BMP protein in conditioned medium was measured by either Western blot analysis or by

analyzing protein secreted from ³⁵S-methionine labelled cells by PAGE and fluorography. The amount of activity produced by the same cell lines on W20 cells using either the alkaline phosphatase assay or osteocalcin-induction assay was then estimated. The specific activity of the BMP was calculated from the ratio of activity to protein secreted into the growth medium.

In one experiment 2E7E-10 and 2EG5 secreted similar amounts of total BMP proteins as determined by PAGE and fluorography. 2E7E-10 produced about 50-fold more alkaline phosphatase inducing activity than the 2EG5, suggesting that the specific activity of the heterodimer is about 50-fold higher than the homodimer.

In another experiment the amount of BMP-2 secreted by 2EG5 was about 50% higher than BMP-2/7 secreted by 2E7E-10, however, 2E7E-10 produced about 10-fold more osteocalcin-inducing activity than 2EG5. From several different experiments of this type the specific activity of the BMP-2/7 heterodimer is estimated to be between 5 to 50 fold higher than the BMP-2 homodimer.

Figures 8 and 9 compare the activity of BMP-2 and BMP-2/7 in the W20 alkaline phosphatase and BGP (Bone Gla Protein, osteocalcin) assays. BMP-2/7 has greatly increased specific activity relative to BMP-2 (Figure 8). From Figure 8, approximately 1.3 ng/ml of BMP-2/7 was sufficient to induce 50% of the maximal alkaline phosphatase response in W-20 cells. A comparable value

for BMP-2 is difficult to calculate, since the alkaline phosphatase response did not maximize, but greater than 30 ng/ml is needed for a half-maximal response. BMP-2/7 thus has a 20 to 30-fold higher specific activity than BMP-2 in the W-20 assay.

As seen in Figure 9, BMP-2/7 was also a more effective stimulator of BGP (bone gla protein, osteocalcin) production than BMP-2 in this experiment. Treating W-20-17 cells with BMP-2/7 for four days resulted in a maximal BGP response with 62 ng/ml, and 11 ng/ml elicits 50% of the maximal BGP response. In contrast, maximal stimulation of BGP synthesis by BMP-2 was not seen with doses up to 468 ng/ml of protein. The minimal dose of BMP-2/7 needed to elicit a BGP response by W-20-17 cells was 3.9 ng/ml, about seven-fold less than the 29 ng/ml required of BMP-2. These results were consistent with the data obtained in the W-20-17 alkaline phosphatase assays for BMP-2 and BMP-2/7.

Preliminary analysis indicates that BMP-2/6 has a specific activity in vitro similar to that of BMP-2/7. The potencies of BMP-2 and BMP-2/6 on induction of alkaline phosphatase production in W-20 is compared, as shown in Figure 12, BMP-2/6 has a higher specific activity than BMP-2 in this assay system. This data is in good agreement with data obtained from the *in vivo* assay of BMP-2 and BMP-2/6).

B. In Vivo Assay**(i) BMP-2/7**

The purified BMP-2/7 and BMP-2 were tested in the rat ectopic bone formation assay. A series of different amounts of BMP-2/7 or BMP-2 were implanted in triplicate in rats. After 5 and 10 days, the implants were removed and examined histologically for the presence of bone and cartilage. The histological scores for the amounts of new cartilage and bone formed are summarized in Table A.

Table A

		5 Day Implants		10 Day Implants	
		BMP-2/7	BMP-2	BMP-2/7	BMP-2
0.04	C	$\pm - \pm$	---	$\pm - \pm$	---
	B	---	---	$\pm - \pm$	---
0.02	C	$\pm 1 \pm$	---	2 1 2	- $\pm \pm$
	B	---	---	1 ± 1	- $\pm -$
1.0	C	1 $\pm \pm$	$\pm \pm \pm$	2 2 2	1 1 \pm
	B	---	---	2 3 3	1 1 \pm
5.0	C	2 2 1	1 ± 1	1 1 2	1 2 1
	B	$\pm - 1$	---	4 4 3	2 3 2
25.0	C			$\pm \pm 2$	2 2 2
	B			4 4 3	3 3 3

The amount of BMP-2/7 required to induce cartilage and bone in the rat ectopic assay is lower than that of BMP-2. Histologically, the appearance of cartilage and bone induced by BMP-2/7 and BMP-2 are identical.

5 (ii) BMP-2/6

The *in vivo* activity of BMP-2/6 was compared with that of BMP-2 by implantation of various amounts of each BMP for ten days in the rat ectopic bone formation assay. The results of this study (Table B, Figure 13) indicate that BMP-2/6, similar to BMP-2/7, has increased *in vivo* activity relative to BMP-2. The specific activities of BMP-2, BMP-6, and BMP-2/6 are compared in the ectopic bone formation assay ten days after the proteins are implanted. The results of these experiments are shown in Table C and Figure 14. BMP-2/6 is a more potent inducer of bone formation than either BMP-2 or BMP-6. The amount

of bone formation observed with BMP-2/6 was comparable to that observed with equivalent doses of BMP-2/7. The appearance of BMP-2/6 implants is quite similar to implants containing BMP-2 or BMP-2/7.

5

Table B

Histological scores of Implants of BMP 2/6 and BMP-2 In rat ectopic assay (10 day implants).

	BMP (μ g)	C/B	BMP-2/6			BMP-2		
10	0.04	C	-	±	-	-	-	-
		B	-	-	-	-	-	-
	0.20	C	1	1	±	-	-	-
		B	±	±	±	-	-	-
	1.0	C	1	3	3	1	1	±
		B	1	2	2	1	1	±
	5.0	C	2	2	2	1	2	2
		B	2	3	3	2	2	2
	25.	C	1	1	1	2	2	1
		B	3	3	3	3	3	3

15

Table C

Histological scores of implants of BMP-2, BMP-6, and BMP-2/6 in rat ectopic assay (10 day implants).

	BMP (μ g)	C/B	BMP-2			BMP-6			BMP-2/6		
20	0.04	C	-	-	-	-	-	-	-	-	±
		B	-	-	-	-	-	-	-	-	±
	0.20	C	-	-	2	-	-	-	1	2	2
		B	-	-	1	-	-	-	2	2	2
	1.0	C	-	±	±	2	1	1	1	1	1
		B	-	±	±	1	±	±	3	3	2
	5.0	C	2	2	1	3	1	3	±	±	1
		B	1	1	1	2	±	1	4	5	4
	25.	C	±	±	±	±	±	±	±	±	±
		B	5	4	5	4	4	5	4	5	3

EXAMPLE 7 - EXPRESSION OF BMP DIMER IN E. COLI

A biologically active, homodimeric BMP-2 was expressed in E. coli using the techniques described in

European Patent Application 433,255 with minor modifications. Other methods disclosed in the above-referenced European patent application may also be employed to produce heterodimers of the present invention from E. coli. Application of these methods to the heterodimers of this invention is anticipated to produce active BMP heterodimeric proteins from E. coli.

A. BMP-2 Expression Vector

An expression plasmid pALBP2-781 (Figure 7) (SEQ ID NO: 13) was constructed containing the mature portion of the BMP-2 (SEQ ID NO: 14) gene and other sequences which are described in detail below. This plasmid directed the accumulation of 5-10% of the total cell protein as BMP-2 in an E. coli host strain, GI724, described below.

Plasmid pALBP2-781 contains the following principal features. Nucleotides 1-2060 contain DNA sequences originating from the plasmid pUC-18 [Norrrander et al, Gene, 26:101-106 (1983)] including sequences containing the gene for β -lactamase which confers resistance to the antibiotic ampicillin in host E. coli strains, and a colE1-derived origin of replication. Nucleotides 2061-2221 contain DNA sequences for the major leftward promoter (pL) of bacteriophage λ [Sanger et al, J. Mol. Biol., 162:729-773 (1982)], including three operator sequences, O_L1, O_L2 and O_L3. The operators are the binding sites for λ cI repressor protein,

intracellular levels of which control the amount of transcription initiation from pL. Nucleotides 2222-2723 contain a strong ribosome binding sequence included on a sequence derived from nucleotides 35566 to 35472 and
5 38137 to 38361 from bacteriophage lambda as described in Sanger et al, J. Mol. Biol., 162:729-773 (1982). Nucleotides 2724-3133 contain a DNA sequence encoding mature BMP-2 protein with an additional 62 nucleotides of 3'-untranslated sequence.

10 Nucleotides 3134-3149 provide a "Linker" DNA sequence containing restriction endonuclease sites. Nucleotides 3150-3218 provide a transcription termination sequence based on that of the E. coli aspA gene [Takagi et al, Nucl. Acids Res., 13:2063-2074 (1985)].
15 Nucleotides 3219-3623 are DNA sequences derived from pUC-18.

As described below, when cultured under the appropriate conditions in a suitable E. coli host strain, pALBP2-781 can direct the production of high
20 levels (approximately 10% of the total cellular protein) of BMP-2 protein.

pALBP2-781 was transformed into the E. coli host strain GI724 (F, lacI^q, lacP^{L8}, ampC::λcI⁺) by the procedure of Dagert and Ehrlich, Gene, 6:23 (1979). [The
25 untransformed host strain E. coli GI724 was deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland on January 31, 1991 under ATCC

No. 55151 for patent purposes pursuant to applicable laws and regulations.] Transformants were selected on 1.5% w/v agar plates containing IMC medium, which is composed of M9 medium [Miller, "Experiments in Molecular Genetics", Cold Spring Harbor Laboratory, New York (1972)] supplemented with 0.5% w/v glucose, 0.2% w/v casamino acids and 100 µg/ml ampicillin.

GI724 contains a copy of the wild-type λ cI repressor gene stably integrated into the chromosome at the ampC locus, where it has been placed under the transcriptional control of Salmonella typhimurium trp promoter/operator sequences. In GI724, λ cI protein is made only during growth in tryptophan-free media, such as minimal media or a minimal medium supplemented with casamino acids such as IMC, described above. Addition of tryptophan to a culture of GI724 will repress the trp promoter and turn off synthesis of λ cI, gradually causing the induction of transcription from pL promoters if they are present in the cell.

GI724 transformed with pALBP2-781 was grown at 37°C to an A_{550} of 0.5 (Absorbance at 550 nm) in IMC medium. Tryptophan was added to a final concentration of 100 µg/ml and the culture incubated for a further 4 hours. During this time BMP-2 protein accumulated to approximately 10% of the total cell protein, all in the "inclusion body" fraction.

BMP-2 is recovered in a non-soluble,

monomeric form as follows. Cell disruption and recovery is performed at 4°C. Approximately 9 g of the wet fermented E. coli GI724/pALBP2-781 cells are suspended in 30 mL of 0.1 M Tris/HCl, 10 mM EDTA, 1 mM phenyl methyl sulphonyl fluoride (PMSF), pH 8.3 (disruption buffer). The cells are passed four times through a cell disrupter and the volume is brought to 100 mL with the disruption buffer. The suspension is centrifuged for 20 min. (15,000 x g). The pellet obtained is suspended in 50 mL disruption buffer containing 1 M NaCl and centrifuged for 10 min. as above. The pellet is suspended in 50 mL disruption buffer containing 1% Triton X-100 (Pierce) and again centrifuged for 10 min. as above. The washed pellet is then suspended in 25 mL of 20 mM Tris/HCl, 1 mM EDTA, 1 mM PMSF, 1% DTT, pH 8.3 and homogenized in a glass homogenizer. The resulting suspension contains crude monomeric BMP-2 in a non-soluble form.

Ten mL of the BMP-2 suspension, obtained as described above, are acidified with 10% acetic acid to pH 2.5 and centrifuged in an Eppendorf centrifuge for 10 min. at room temperature. The supernatant is chromatographed. Chromatography was performed on a Sephacryl S-100 HR column (Pharmacia, 2.6 x 83 cm) in 1% acetic acid at a flow rate of 1.4 mL/minute. Fractions containing monomeric, BMP-2 are pooled. This material is used to generate biologically active, homodimer BMP-2.

Biologically active, homodimeric BMP-2 can

be generated from the monomeric BMP-2 obtained following solubilization and purification, described above, as follows.

0.1, 0.5 or 2.5 mg of the BMP-2 is dissolved at a concentration of 20, 100 or 500 μ g/mL, respectively, in 50 mM Tris/HCl, pH 8.0, 1 M NaCl, 5 mM EDTA, 2 mM reduced glutathione, 1 mM oxidized glutathione and 33 mM CHAPS [Calbiochem]. After 4 days at 4°C or 23°C, the mixture is diluted 5 to 10 fold with 0.1% TFA.

Purification of biologically active BMP-2 is achieved by subjecting the diluted mixture to reverse phase HPLC on a a Vydac C4 214TP54 column (25 x .46 cm) [The NEST Group, USA] at a flow rate of 1 ml/minute. Buffer A is 0.1% TFA. Buffer B is 90% acetonitrile, and 0.1% TFA. The linear gradient was 0 to 5 minutes at 20% Buffer B; 5 to 10 minutes at 20 to 30 % Buffer B; 10 to 40 minutes at 30 to 60% Buffer B; and 40 to 50 minutes at 60 to 100% Buffer B. Homodimeric BMP-2 is eluted and collected from the HPLC column.

The HPLC fractions are lyophilized to dryness, redissolved in sample buffer (1.5 M Tris-HCl, pH 8.45, 12% glycerol, 4% SDS, .0075% Serva Blue G, .0025% Phenol Red, with or without 100 mM dithiothreitol) and heated for five minutes at 95°C. The running buffer is 100 mM Tris, 100 mM tricine (16% tricine gel) [Novex], 0.1% SDS at pH 8.3. The SDS-PAGE gel is run at 125 volts for 2.5 hours.

The gel is stained for one hour with 200 ml of 0.5% Coomassie Brilliant Blue R-250, 25% isopropanol, 10% acetic acid, heated to 60°C. The gel is then destained with 10% acetic acid, 10% isopropanol
5 until the background is clear.

The reduced material ran at approximately 13kD; the non-reduced material ran at approximately 30 kD, which is indicative of the BMP-2 dimer. This material was later active in the W20 assay of Example 8.

10 B. BMP-7 Expression Vector

For high level expression of BMP-7 a plasmid pALBMP7-981 was constructed. pALBMP7-981 is identical to plasmid pALBP2-781 with two exceptions: the BMP-2 gene (residues 2724-3133 of pALBP2-781) is replaced
15 by the mature portion of the BMP-7 gene, deleted for sequenced encoding the first seven residues of the mature BMP-7 protein sequence:

ATGTCTCATAATC GTTCTAAAAC TCCAAAAAAT CAAGAAGCTC TCGGTATGGC

CAACGTGGCA GAGAACAGCA GCAGCGACCA GAGGCAGGCC TGTAAAGAAGC
 ACGAGCTGTA TGTCAGCTTC CGAGACCTGG GCTGGCAGGA CTGGATCATC
 GCGCCTGAAG GCTACGCCGC CTACTACTGT GAGGGGGAGT GTGCCTTCCC
 5 TCTGAACTCC TACATGAACG CCACCAACCA CGCCATCGTG CAGACGCTGG
 TCCACTTCAT CAACCCGGAA ACGGTGCCCA AGCCCTGCTG TGCGCCCACG
 CAGCTCAATG CCATCTCCGT CCTCTACTTC GATGACAGCT CCAACGTCAT
 CCTGAAGAAA TACAGAAACA TGGTGGTCCG GGCCTGTGGC TGCCACTAGC
 TCCTCCGAGA ATTCAGACCC TTTGGGGCCA AGTTTTTCTG GATCCT

10 and the ribosome binding site found between residues
 2707 and 2723 in pALBP2-781 is replaced by a different
 ribosome binding site, based on that found preceding the
 T7 phage gene 10, of sequence 5'-CAAGAAGGAGATATACAT-3'.
 The host strain and growth conditions used for the
 15 production of BMP-7 were as described for BMP-2.

C. BMP-3 Expression Vector

For high level expression of BMP-3 a
 plasmid pALB3-782 was constructed. This plasmid is
 identical to plasmid pALBP2-781, except that the BMP-2
 20 gene (residues 2724-3133 of pALBP2-781) is replaced by a
 gene encoding a form of mature BMP-3. The sequence of
 this BMP-3 gene is:

80

ATGCGTAAAC AATGGATTGA ACCACGTAAC TGTGCTCGTC GTTATCTGAA
AGTAGACTTT GCAGATATTG GCTGGAGTGA ATGGATTATC TCCCCCAAGT
CCTTTGATGC CTATTATTGC TCTGGAGCAT GCCAGTTCCC CATGCCAAAG
TCTTTGAAGC CATCAAATCA TGCTACCATC CAGAGTATAG TGAGAGCTGT
5 GGGGGTCGTT CCTGGGATTG CTGAGCCTTG CTGTGTACCA GAAAAGATGT
CCTCACTCAG TATTTTATTC TTTGATGAAA ATAAGAATGT AGTGCTTAAA
GTATACCCTA ACATGACAGT AGAGTCTTGC GCTTGCAGAT AACCTGGCAA
AGAACTCATT TGAATGCTTA ATTCAAT

The host strain and growth conditions used for the
10 production of BMP-3 were as described for BMP-2.

D. Expression of a BMP-2/7 Heterodimer in E. coli

Denatured and purified E. coli BMP-2 and BMP-7
monomers were isolated from E. coli inclusion body
15 pellets by acidification and gel filtration as previously
as previously described above. 125 ug of each BMP in 1%
acetic acid were mixed and taken to dryness in a speed
vac. The material was resuspended in 2.5 ml 50 mM Tris,
1.0 NaCl, 5 mM EDTA, 33 mM CHAPS, 2 mM glutathione
20 (reduced), 1 mM glutathione (oxidized), pH 8.0. The
sample was incubated at 23 C for one week.

The BMP-2/7 heterodimer was isolated by
HPLC on a 25 x 0.46 cm Vydac C4 column. The sample was
centrifuged in a microfuge for 5 minutes, and the
25 supernatant was diluted with 22.5 ml 0.1% TFA.

A buffer : 0.1% TFA

B buffer : 0.1% TFA, 95% acetonitrile

81

1.0 ml/minute

0-5' 20% B

5-10' 20-30% B

10-90' 30-50% B

5 90-100' 50-100% B

By SDS-PAGE analysis, the BMP-2/7 heterodimer eluted at about 23'.

Figure 10 is a comparison of the W-20 activity of E. coli BMP-2 and BMP-2/7 heterodimer, indicating greater activity of the heterodimer.

F. Expression of BMP-2/3 Heterodimer in E. coli

BMP-2 and BMP-3 monomers were isolated as follows: to 1.0 g of frozen harvested cells expressing either BMP-2 or BMP-3 was added 3.3 ml of 100 mM Tris, 10 mM EDTA, pH 8.3. The cells were resuspended by vortexing vigorously. 33 ul of 100 mM PMSF in isopropanol was added and the cells lysed by one pass through a French pressure cell. The lysate was centrifuged in a microfuge for 20 minutes at 4 C. The supernatant was discarded. The inclusion body pellet was taken up in 8.0 M guanidine hydrochloride, 0.25 M OTT, 0.5 M Tris, 5 mM EDTA, pH 8.5, and heated at 37 C for one hour.

The reduced and denatured BMP monomers were isolated by HPLC on a Supelco C4 guard column as follows:

A buffer : 0.1% TFA

B buffer : 0.1% TFA, 95% acetonitrile

82

1.0 ml/minute

0-5' 1% B

5-40' 1-70% B

40-45' 70-100% B

5 Monomeric BMP eluted at 28-30'. Protein concentration was estimated by A280 and the appropriate extinction coefficient.

10 10 ug of BMP-2 and BMP-3 were combined and taken to dryness in a speed vac. To this was added 50 ul of 50 mM Tris, 1.0 M NaCl, 5 mM EDTA, 33 mM CHAPS, 2 mM reduced glutathione, 1 mM oxidized glutathione, pH 8.5. The sample was incubated at 23 for 3 days. The sample was analyzed by SDS-PAGE on a 16% tricine gel under reducing and nonreducing conditions. The BMP-2/3 heterodimer
15 migrated at about 35 kd nonreduced, and reduced to BMP-2 monomer at about 13 kd and BMP-3 monomer at about 21 kd.

BMP-2/3 heterodimer produced in *E. coli* is tested for *in vivo* activity. (20 μ g) at (ten days) is utilized to compare the *in vivo* activity of BMP-2/3 to
20 BMP-2. BMP-2/3 implants showed no cartilage or bone forming activity, while the BMP-2 control implants showed the predicted amounts of bone and cartilage formation. The *in vivo* data obtained with BMP-2/3 is consistent with the *in vitro* data from the W-20 assay.

EXAMPLE 8 - W-20 BIOASSAYSA. Description of W-20 cells

Use of the W-20 bone marrow stromal cells as an indicator cell line is based upon the conversion of these cells to osteoblast-like cells after treatment with BMP-2 [R. S. Thies et al, "Bone Morphogenetic Protein alters W-20 stromal cell differentiation in vitro", Journal of Bone and Mineral Research, 5(2):305 (1990); and R. S. Thies et al, "Recombinant Human Bone Morphogenetic Protein 2 Induces Osteoblastic Differentiation in W-20-17 Stromal Cells", Endocrinology, in press (1992)]. Specifically, W-20 cells are a clonal bone marrow stromal cell line derived from adult mice by researchers in the laboratory of Dr. D. Nathan, Children's Hospital, Boston, MA. BMP-2 treatment of W-20 cells results in (1) increased alkaline phosphatase production, (2) induction of PTH stimulated cAMP, and (3) induction of osteocalcin synthesis by the cells. While (1) and (2) represent characteristics associated with the osteoblast phenotype, the ability to synthesize osteocalcin is a phenotypic property only displayed by mature osteoblasts. Furthermore, to date we have observed conversion of W-20 stromal cells to osteoblast-like cells only upon treatment with BMPs. In this manner, the in vitro activities displayed by BMP treated W-20 cells correlate with the in vivo bone forming activity known for BMPs.

Below two in vitro assays useful in comparison of BMP activities of novel osteoinductive molecules are described.

B. W-20 Alkaline Phosphatase Assay Protocol

5 W-20 cells are plated into 96 well tissue culture plates at a density of 10,000 cells per well in 200 μ l of media (DME with 10% heat inactivated fetal calf serum, 2 mM glutamine and 100 U/ml + 100 μ g/ml streptomycin. The cells are allowed to attach overnight
10 in a 95% air, 5% CO₂ incubator at 37°C.

 The 200 μ l of media is removed from each well with a multichannel pipettor and replaced with an equal volume of test sample delivered in DME with 10% heat inactivated fetal calf serum, 2 mM glutamine and 1%
15 penicillin-streptomycin. Test substances are assayed in triplicate.

 The test samples and standards are allowed a 24 hour incubation period with the W-20 indicator cells. After the 24 hours, plates are removed from the
20 37°C incubator and the test media are removed from the cells.

 The W-20 cell layers are washed 3 times with 200 μ l per well of calcium/magnesium free phosphate buffered saline and these washes are discarded.

25 50 μ l of glass distilled water is added to each well and the assay plates are then placed on a dry ice/ethanol bath for quick freezing. Once frozen, the

assay plates are removed from the dry ice/ethanol bath and thawed at 37°C. This step is repeated 2 more times for a total of 3 freeze-thaw procedures. Once complete, the membrane bound alkaline phosphatase is available for measurement.

50 µl of assay mix (50 mM glycine, 0.05% Triton X-100, 4 mM MgCl₂, 5 mM p-nitrophenol phosphate, pH = 10.3) is added to each assay well and the assay plates are then incubated for 30 minutes at 37°C in a shaking waterbath at 60 oscillations per minute.

At the end of the 30 minute incubation, the reaction is stopped by adding 100 µl of 0.2 N NaOH to each well and placing the assay plates on ice.

The spectrophotometric absorbance for each well is read at a wavelength of 405 nanometers. These values are then compared to known standards to give an estimate of the alkaline phosphatase activity in each sample. For example, using known amounts of p-nitrophenol phosphate, absorbance values are generated. This is shown in Table I.

Table I

Absorbance Values for Known Standards
of P-Nitrophenol Phosphate

<u>P-nitrophenol phosphate umoles</u>	<u>Mean absorbance (405 nm)</u>
0.000	0
0.006	0.261 +/- .024
0.012	0.521 +/- .031
0.018	0.797 +/- .063

86

0.024
0.030

1.074 +/- .061
1.305 +/- .083

Absorbance values for known amounts of
5 BMP-2 can be determined and converted to μ moles of p-
nitrophenol phosphate cleaved per unit time as shown in
Table II.

Table II

10 Alkaline Phosphatase Values for W-20 Cells
Treating with BMP-2

	BMP-2 concentration ng/ml	Absorbance Reading 405 nmeters	umoles substrate per hour
	0	0.645	0.024
15	1.56	0.696	0.026
	3.12	0.765	0.029
	6.25	0.923	0.036
	12.50	1.121	0.044
	25.0	1.457	0.058
20	50.0	1.662	0.067
	100.0	1.977	0.080

These values are then used to compare the
activities of known amounts of BMP heterodimers to BMP-2
25 homodimer.

C. Osteocalcin RIA Protocol

W-20 cells are plated at 10^6 cells per well
in 24 well multiwell tissue culture dishes in 2 mls of
DME containing 10% heat inactivated fetal calf serum, 2
30 mM glutamine. The cells are allowed to attach overnight
in an atmosphere of 95% air 5% CO₂ at 37°C.

The next day the medium is changed to DME

containing 10% fetal calf serum, 2 mM glutamine and the test substance in a total volume of 2 ml. Each test substance is administered to triplicate wells. The test substances are incubated with the W-20 cells for a total of 96 hours with replacement at 48 hours by the same test medias.

At the end of 96 hours, 50 μ l of the test media is removed from each well and assayed for osteocalcin production using a radioimmunoassay for mouse osteocalcin. The details of the assay are described in the kit manufactured by Biomedical Technologies Inc., 378 Page Street, Stoughton, MA 02072. Reagents for the assay are found as product numbers BT-431 (mouse osteocalcin standard), BT-432 (Goat anti-mouse Osteocalcin), BT-431R (iodinated mouse osteocalcin), BT-415 (normal goat serum) and BT-414 (donkey anti goat IgG). The RIA for osteocalcin synthesized by W-20 cells in response to BMP treatment is carried out as described in the protocol provided by the manufacturer.

The values obtained for the test samples are compared to values for known standards of mouse osteocalcin and to the amount of osteocalcin produced by W-20 cells in response to challenge with known amounts of BMP-2. The values for BMP-2 induced osteocalcin synthesis by W-20 cells is shown in Table III.

Table III

Osteocalcin Synthesis by W-20 Cells

	<u>BMP-2 Concentration ng/ml</u>	<u>Osteocalcin Synthesis ng/well</u>
5	0	0.8
	2	0.9
	4	0.8
	8	2.2
	16	2.7
10	31	3.2
	62	5.1
	125	6.5
	250	8.2
	500	9.4
15	1000	10.0

EXAMPLE 9 - ROSEN MODIFIED SAMPATH-REDDI ASSAY

A modified version of the rat bone formation assay described in Sampath and Reddi, Proc. Natl. Acad. Sci. USA, 80:6591-6595 (1983) is used to evaluate bone and/or cartilage activity of BMP proteins. This modified assay is herein called the Rosen-modified Sampath-Reddi assay. The ethanol precipitation step of the Sampath-Reddi procedure is replaced by dialyzing (if the composition is a solution) or diafiltering (if the composition is a suspension) the fraction to be assayed against water. The solution or suspension is then redissolved in 0.1% TFA, and the resulting solution added to 20 mg of rat matrix. A mock rat matrix sample not treated with the protein serves as a control. This material is frozen and lyophilized and the resulting powder enclosed in #5 gelatin capsules. The capsules are

implanted subcutaneously in the abdominal thoracic area of 21-49 ay old male Long Evans rats. The implants are removed after 7-14 days. Half of each implant is used for alkaline phosphatase analysis [see, A. H. Reddi et al, Proc. Natl. Acad. Sci., 69:1601 (1972)].

The other half of each implant is fixed and processed for histological analysis. 1 μ m glycolmethacrylate sections are stained with Von Kossa and acid fuschin to score the amount of induced bone and cartilage formation present in each implant. The terms +1 through +5 represent the area of each histological section of an implant occupied by new bone and/or cartilage cells and matrix. A score of +5 indicates that greater than 50% of the implant is new bone and/or cartilage produced as a direct result of protein in the implant. A score of +4, +3, +2, and +1 would indicate that greater than 40%, 30%, 20% and 10% respectively of the implant contains new cartilage and/or bone.

The heterodimeric BMP proteins of this invention may be assessed for activity on this assay.

Numerous modifications and variations in practice of this invention are expected to occur to those skilled in the art. Such modifications and variations are encompassed within the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Israel, David
Wolfman, Neil M.
- (ii) TITLE OF INVENTION: Recombinant Bone Morphogenetic Protein
Heterodimers, Compositions and Methods of Use.
- (iii) NUMBER OF SEQUENCES: 30
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140-2387
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Tape
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kapinos, Ellen J.
 - (B) REGISTRATION NUMBER: 32,245
 - (C) REFERENCE/DOCKET NUMBER: GI-5192B
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-876-1170
 - (B) TELEFAX: 617-876-5851

:) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1607 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 356..1543
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT	60
AACTTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT	120
CCGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCCGAC ACTGAGACGC TGTTCCCAGC	180
GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG	240
GACATTCCGGT CCTTGCGCCA GGTCCCTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA	300
ATGGACGTGT CCCC GCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG Met 1	358
GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu 5 10 15	406
CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe 20 25 30	454
GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val 35 40 45	502
CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln 50 55 60 65	550
AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp 70 75 80	598
CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp His 85 90 95	646
CGG TTG GAG AGG GCA GCC AGC CGA GCC AAC ACT GTG CGC AGC TTC CAC Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe His 100 105 110	694
CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG AGT GGG AAA ACA ACC His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr Thr 115 120 125	742
CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG GAG TTT ATC Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile 130 135 140 145	790
ACC TCA GCA GAG CTT CAG GTT TTC CGA GAA CAG ATG CAA GAT GCT TTA Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala Leu 150 155 160	838
GGA AAC AAT AGC AGT TTC CAT CAC CGA ATT AAT ATT TAT GAA ATC ATA Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile 165 170 175	886
AAA CCT GCA ACA GCC AAC TCG AAA TTC CCC GTG ACC AGA CTT TTG GAC Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp	934

92																
180					185					190						
ACC	AGG	TTG	GTG	AAT	CAG	AAT	GCA	AGC	AGG	TGG	GAA	ACT	TTT	GAT	GTC	982
Thr	Arg	Leu	Val	Asn	Gln	Asn	Ala	Ser	Arg	Trp	Glu	Thr	Phe	Asp	Val	
	195					200					205					
ACC	CCC	GCT	GTG	ATG	CGG	TGG	ACT	GCA	CAG	GGA	CAC	GCC	AAC	CAT	GGA	1030
Thr	Pro	Ala	Val	Met	Arg	Trp	Thr	Ala	Gln	Gly	His	Ala	Asn	His	Gly	
	210				215					220					225	
TTC	GTG	GTG	GAA	GTG	GCC	CAC	TTG	GAG	GAG	AAA	CAA	GGT	GTC	TCC	AAG	1078
Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	Lys	Gln	Gly	Val	Ser	Lys	
				230					235					240		
AGA	CAT	GTT	AGG	ATA	AGC	AGG	TCT	TTG	CAC	CAA	GAT	GAA	CAC	AGC	TGG	1126
Arg	His	Val	Arg	Ile	Ser	Arg	Ser	Leu	His	Gln	Asp	Glu	His	Ser	Trp	
			245					250					255			
TCA	CAG	ATA	AGG	CCA	TTG	CTA	GTA	ACT	TTT	GGC	CAT	GAT	GGA	AAA	GGG	1174
Ser	Gln	Ile	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly	His	Asp	Gly	Lys	Gly	
		260				265						270				
CAT	CCT	CTC	CAC	AAA	AGA	GAA	AAA	CGT	CAA	GCC	AAA	CAC	AAA	CAG	CGG	1222
His	Pro	Leu	His	Lys	Arg	Glu	Lys	Arg	Gln	Ala	Lys	His	Lys	Gln	Arg	
	275					280					285					
AAA	CGC	CTT	AAG	TCC	AGC	TGT	AAG	AGA	CAC	CCT	TTG	TAC	GTG	GAC	TTC	1270
Lys	Arg	Leu	Lys	Ser	Ser	Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	
	290				295					300					305	
AGT	GAC	GTG	GGG	TGG	AAT	GAC	TGG	ATT	GTG	GCT	CCC	CCG	GGG	TAT	CAC	1318
Ser	Asp	Val	Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	His	
				310					315					320		
GCC	TTT	TAC	TGC	CAC	GGA	GAA	TGC	CCT	TTT	CCT	CTG	GCT	GAT	CAT	CTG	1366
Ala	Phe	Tyr	Cys	His	Gly	Glu	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	
			325					330					335			
AAC	TCC	ACT	AAT	CAT	GCC	ATT	GTT	CAG	ACG	TTG	GTC	AAC	TCT	GTT	AAC	1414
Asn	Ser	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	
			340				345					350				
TCT	AAG	ATT	CCT	AAG	GCA	TGC	TGT	GTC	CCG	ACA	GAA	CTC	AGT	GCT	ATC	1462
Ser	Lys	Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	
	355					360					365					
TCG	ATG	CTG	TAC	CTT	GAC	GAG	AAT	GAA	AAG	GTT	GTA	TTA	AAG	AAC	TAT	1510
Ser	Met	Leu	Tyr	Leu	Asp	Glu	Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	
	370				375					380					385	
CAG	GAC	ATG	GTT	GTG	GAG	GGT	TGT	GGG	TGT	CGC	TAGTACAGCA AAATTAAATA					1563
Gln	Asp	Met	Val	Val	Glu	Gly	Cys	Gly	Cys	Arg						
				390				395								
CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAA															1607	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 396 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val
 1           5           10           15
Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys
          20           25           30
Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
          35           40           45
Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
          50           55           60
Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
          65           70           75           80
Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
          85           90           95
His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
          100          105          110
His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
          115          120          125
Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
          130          135          140
Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
          145          150          155          160
Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
          165          170          175
Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
          180          185          190
Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Thr Phe Asp
          195          200          205
Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
          210          215          220
Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
          225          230          235          240
Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
          245          250          255
Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
          260          265          270
Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln

```

94

275	280	285
Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp 290 295 300		
Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr 305 310 315 320		
His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His 325 330 335		
Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val 340 345 350		
Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala 355 360 365		
Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn 370 375 380		
Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg 385 390 395		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 403..1626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA	60
GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG	120
AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC	180
ACAGTCCCCG GCCCTCGCCC AGGTTCACTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG	240
CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC	300
GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG CTGTCAAGAA	360
TCATGGACTG TTATTATATG CCTTGTTTTT TGTCAAGACA CC ATG ATT CCT GGT	414
	Met Ile Pro Gly
	1
AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC	462
Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly	
5 10 15 20	

95

CGC AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala	510
25 30 35	
GAG ATT CAG GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu	558
40 45 50	
CTC CTG CCG GAC TTC GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met Phe Gly Leu Arg	606
55 60 65	
CGC CGC CCG CAG CCT AGC AAG AGT GCC GTC ATT CCG GAC TAC ATG CGG Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro Asp Tyr Met Arg	654
70 75 80	
GAT CTT TAC CCG CTT CAG TCT GGG GAG GAG GAG GAA GAG CAG ATC CAC Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu Gln Ile His	702
85 90 95 100	
AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC AGC CCG GCC AAC ACC Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser Arg Ala Asn Thr	750
105 110 115	
GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC CCA GGG ACC Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile Pro Gly Thr	798
120 125 130	
AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC CCT Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile Pro	846
135 140 145	
GAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CCG GAG CAG Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln	894
150 155 160	
GTG GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile	942
165 170 175 180	
TAT GAG GTT ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile	990
185 190 195	
ACA CGA CTA CTG GAC ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn Val Thr Arg Trp	1038
200 205 210	
GAA ACT TTT GAT GTG AGC CCT GCG GTC CTT CGC TGG ACC CGG GAG AAG Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp Thr Arg Glu Lys	1086
215 220 225	
CAG CCA AAC TAT GGG CTA GCC ATT GAG GTG ACT CAC CTC CAT CAG ACT Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His Leu His Gln Thr	1134
230 235 240	
CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC CGA TCG TTA CCT CAA Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln	1182
245 250 255 260	

96

GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC ACC TTT GGC Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly 265 270	1230
CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG CGT His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Arg Ala Lys Arg 280 285 290	1278
AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys 295 300 305	1326
CGG CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp 310 315 320	1374
TGG ATT GTG GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGG GAC Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp 325 330 335 340	1422
TGC CCC TTT CCA CTG GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile 345 350 355	1470
GTG CAG ACC CTG GTC AAT TCT GTC AAT TCC AGT ATC CCC AAA GCC TGT Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys 360 365 370	1518
TGT GTG CCC ACT GAA CTG AGT GCC ATC TCC ATG CTG TAC CTG GAT GAG Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu 375 380 385	1566
TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG ATG GTA GTA GAG GGA Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly 390 395 400	1614
TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG ATATACACAC Cys Gly Cys Arg 405	1666
CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC	1726
ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAAAAA AATGGAAAAA	1786
ATCCCTAAAC ATTACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT	1846
TGATCATATA TTTTGACAAA ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG	1906
AGTCATTATT TTAATAAAAAA AAAAAAACT CTAGAGTCGA CGGAATTC	1954

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
 1 5 10 15
 Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
 20 25 30
 Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
 35 40 45
 Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
 50 55 60
 Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
 65 70 75 80
 Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
 85 90 95
 Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
 100 105 110
 Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
 115 120 125
 Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
 130 135 140
 Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu
 145 150 155 160
 Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
 165 170 175
 Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
 180 185 190
 Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
 195 200 205
 Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
 210 215 220
 Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
 225 230 235 240
 Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
 245 250 255
 Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
 260 265 270
 Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
 275 280 285
 Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
 290 295 300

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
 305 310 315 320
 Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
 325 330 335
 Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
 340 345 350
 Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
 355 360 365
 Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
 370 375 380
 Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
 385 390 395 400
 Val Val Glu Gly Cys Gly Cys Arg
 405

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..1389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGACCGAGC GCGCGGACG GCCGCCTGCC CCCTCTGCCA CCTGGGGCGG TGCGGGCCCG	60
GAGCCCGGAG CCCGGGTAGC GCGTAGAGCC GGCGCG ATG CAC GTG CGC TCA CTG	114
Met His Val Arg Ser Leu	
1 5	
CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA CCC CTG TTC	162
Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala Pro Leu Phe	
10 15 20	
CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC GAG GTG CAC	210
Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn Glu Val His	
25 30 35	
TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG CGG GAG ATG	258
Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg Arg Glu Met	
40 45 50	
CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC CCG CGC CCG	306
Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro	
55 60 65 70	

CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu 75 80 85	354
TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC GGC CAG GGC Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly 90 95 100	402
TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT CTG Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu 105 110 115	450
GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC ATG GTC ATG Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp Met Val Met 120 125 130	498
AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC CAC CCA CGC Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro Arg 135 140 145 150	546
TAC CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC CCA GAA GGG Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu Gly 155 160 165	594
GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC TAC ATC CGG Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile Arg 170 175 180	642
GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT CAG GTG CTC Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr Gln Val Leu 185 190 195	690
CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC GAC AGC CGT Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu Asp Ser Arg 200 205 210	738
ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC ATC ACA GCC Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp Ile Thr Ala 215 220 225 230	786
ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG GGC CTG CAG Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu Gly Leu Gln 235 240 245	834
CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC AAG TTG GCG Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro Lys Leu Ala 250 255 260	882
GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC TTC ATG GTG Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro Phe Met Val 265 270 275	930
GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC CGG TCC ACG Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile Arg Ser Thr 280 285 290	978
GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC AAG AAC CAG Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys Asn Gln 295 300 305 310	1026

100

GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC AGC GAC CAG	1074
Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser Asp Gln	
315 320 325	
AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC CGA GAC CTG	1122
Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu	
330 335 340	
GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC GCC TAC TAC	1170
Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr	
345 350 355	
TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC ACC	1218
Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn Ala Thr	
360 365 370	
AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC CCG GAA ACG	1266
Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Glu Thr	
375 380 385 390	
GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC GTC	1314
Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val	
395 400 405	
CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA TAC AGA AAC	1362
Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn	
410 415 420	
ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG	1409
Met Val Val Arg Ala Cys Gly Cys His	
425 430	
ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTC	1448

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	His	Val	Arg	Ser	Leu	Arg	Ala	Ala	Ala	Pro	His	Ser	Phe	Val	Ala
1				5					10					15	
Leu	Trp	Ala	Pro	Leu	Phe	Leu	Leu	Arg	Ser	Ala	Leu	Ala	Asp	Phe	Ser
			20					25					30		
Leu	Asp	Asn	Glu	Val	His	Ser	Ser	Phe	Ile	His	Arg	Arg	Leu	Arg	Ser
		35					40					45			
Gln	Glu	Arg	Arg	Glu	Met	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu
	50					55					60				
Pro	His	Arg	Pro	Arg	Pro	His	Leu	Gln	Gly	Lys	His	Asn	Ser	Ala	Pro

65					70	101				75					80
Met	Phe	Met	Leu	Asp	Leu	Tyr	Asn	Ala	Met	Ala	Val	Glu	Glu	Gly	Gly
				85					90					95	
Gly	Pro	Gly	Gly	Gln	Gly	Phe	Ser	Tyr	Pro	Tyr	Lys	Ala	Val	Phe	Ser
			100					105					110		
Thr	Gln	Gly	Pro	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ser	His	Phe	Leu	Thr
		115					120					125			
Asp	Ala	Asp	Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu	His	Asp	Lys
		130					135				140				
Glu	Phe	Phe	His	Pro	Arg	Tyr	His	His	Arg	Glu	Phe	Arg	Phe	Asp	Leu
145					150					155					160
Ser	Lys	Ile	Pro	Glu	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu	Phe	Arg	Ile
				165					170					175	
Tyr	Lys	Asp	Tyr	Ile	Arg	Glu	Arg	Phe	Asp	Asn	Glu	Thr	Phe	Arg	Ile
			180					185					190		
Ser	Val	Tyr	Gln	Val	Leu	Gln	Glu	His	Leu	Gly	Arg	Glu	Ser	Asp	Leu
		195					200					205			
Phe	Leu	Leu	Asp	Ser	Arg	Thr	Leu	Trp	Ala	Ser	Glu	Glu	Gly	Trp	Leu
		210				215					220				
Val	Phe	Asp	Ile	Thr	Ala	Thr	Ser	Asn	His	Trp	Val	Val	Asn	Pro	Arg
225					230					235					240
His	Asn	Leu	Gly	Leu	Gln	Leu	Ser	Val	Glu	Thr	Leu	Asp	Gly	Gln	Ser
				245					250					255	
Ile	Asn	Pro	Lys	Leu	Ala	Gly	Leu	Ile	Gly	Arg	His	Gly	Pro	Gln	Asn
			260					265					270		
Lys	Gln	Pro	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Thr	Glu	Val	His	Phe
			275				280					285			
Arg	Ser	Ile	Arg	Ser	Thr	Gly	Ser	Lys	Gln	Arg	Ser	Gln	Asn	Arg	Ser
			290			295					300				
Lys	Thr	Pro	Lys	Asn	Gln	Glu	Ala	Leu	Arg	Met	Ala	Asn	Val	Ala	Glu
305					310					315					320
Asn	Ser	Ser	Ser	Asp	Gln	Arg	Gln	Ala	Cys	Lys	Lys	His	Glu	Leu	Tyr
				325					330					335	
Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	Pro	Glu
			340					345					350		
Gly	Tyr	Ala	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asn
			355				360					365			
Ser	Tyr	Met	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	His
			370			375					380				
Phe	Ile	Asn	Pro	Glu	Thr	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	Thr	Gln

102

385

390

395

400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
 405 410 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 420 425 430

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Human placenta

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Stratagene catalog #936203 Human placenta cDNA library
- (B) CLONE: BMP6C35

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 160..1701

(ix) FEATURE:

- (A) NAME/KEY: mat peptide
- (B) LOCATION: 1282..1698

(ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 1..2923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCC GAGAGGTGGC	60
GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG GCCTCGCTCC GCCGCTCCAC	120
GCCTCGCGGG ATCCGCGGGG GCAGCCCGGC CGGGCGGGG ATG CCG GGG CTG GGG	174
Met Pro Gly Leu Gly	
-374 -370	
CGG AGG GCG CAG TGG CTG TGC TGG TGG TGG GGG CTG CTG TGC AGC TGC	222
Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly Leu Leu Cys Ser Cys	
-365 -360 -355	
TGC GGG CCC CCG CCG CTG CGG CCG CCC TTG CCC GCT GCC GCG GCC GCC	270

Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala	
-350 -345 -340	
GCC GCC GGG GGG CAG CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG	318
Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr	
-335 -330 -325	
GAG CAG CCG CCG CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CGG	366
Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg	
-320 -315 -310	
CGG CTC AAG ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG	414
Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln Lys Glu Ile Leu Ser	
-305 -300 -295 -290	
GTG CTG GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG	462
Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln	
-285 -280 -275	
CCG CAG CCC CCG GCG CTC CGG CAG CAG GAG GAG CAG CAG CAG CAG CAG	510
Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu Gln Gln Gln Gln Gln	
-270 -265 -260	
CAG CTG CCT CGC GGA GAG CCC CCT CCC GGG CGA CTG AAG TCC GCG CCC	558
Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg Leu Lys Ser Ala Pro	
-255 -250 -245	
CTC TTC ATG CTG GAT CTG TAC AAC GCC CTG TCC GCC GAC AAC GAC GAG	606
Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser Ala Asp Asn Asp Glu	
-240 -235 -230	
GAC GGG GCG TCG GAG GGG GAG AGG CAG CAG TCC TGG CCC CAC GAA GCA	654
Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser Trp Pro His Glu Ala	
-225 -220 -215 -210	
GCC AGC TCG TCC CAG CGT CGG CAG CCG CCC CCG GGC GCC GCG CAC CCG	702
Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro Gly Ala Ala His Pro	
-205 -200 -195	
CTC AAC CGC AAG AGC CTT CTG GCC CCC GGA TCT GGC AGC GGC GGC GCG	750
Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser Gly Ser Gly Gly Ala	
-190 -185 -180	
TCC CCA CTG ACC AGC GCG CAG GAC AGC GCC TTC CTC AAC GAC GCG GAC	798
Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe Leu Asn Asp Ala Asp	
-175 -170 -165	
ATG GTC ATG AGC TTT GTG AAC CTG GTG GAG TAC GAC AAG GAG TTC TCC	846
Met Val Met Ser Phe Val Asn Leu Val Glu Tyr Asp Lys Glu Phe Ser	
-160 -155 -150	
CCT CGT CAG CGA CAC CAC AAA GAG TTC AAG TTC AAC TTA TCC CAG ATT	894
Pro Arg Gln Arg His His Lys Glu Phe Lys Phe Asn Leu Ser Gln Ile	
-145 -140 -135 -130	
CCT GAG GGT GAG GTG GTG ACG GCT GCA GAA TTC CGC ATC TAC AAG GAC	942
Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp	
-125 -120 -115	
TGT GTT ATG GGG AGT TTT AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT	990

Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr																			
-110																			
-105																			
-100																			
CAA GTC TTA CAG GAG CAT CAG CAC AGA GAC TCT GAC CTG TTT TTG TTG																			1038
Gln Val Leu Gln Glu His Gln His Arg Asp Ser Asp Leu Phe Leu Leu																			
-95																			
-90																			
-85																			
GAC ACC CGT GTA GTA TGG GCC TCA GAA GAA GGC TGG CTG GAA TTT GAC																			1086
Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp																			
-80																			
-75																			
-70																			
ATC ACG GCC ACT AGC AAT CTG TGG GTT GTG ACT CCA CAG CAT AAC ATG																			1134
Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn Met																			
-65																			
-60																			
-55																			
-50																			
GGG CTT CAG CTG AGC GTG GTG ACA AGG GAT GGA GTC CAC GTC CAC CCC																			1182
Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro																			
-45																			
-40																			
-35																			
CGA GCC GCA GGC CTG GTG GGC AGA GAC GGC CCT TAC GAT AAG CAG CCC																			1230
Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro																			
-30																			
-25																			
-20																			
TTC ATG GTG GCT TTC TTC AAA GTG AGT GAG GTC CAC GTG CGC ACC ACC																			1278
Phe Met Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr Thr																			
-15																			
-10																			
-5																			
AGG TCA GCC TCC AGC CGG CGC CGA CAA CAG AGT CGT AAT CGC TCT ACC																			1326
Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn Arg Ser Thr																			
1																			
5																			
10																			
15																			
CAG TCC CAG GAC GTG GCG CGG GTC TCC AGT GCT TCA GAT TAC AAC AGC																			1374
Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp Tyr Asn Ser																			
20																			
25																			
30																			
AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG TAT GTG AGT TTC																			1422
Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr Val Ser Phe																			
35																			
40																			
45																			
CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA CCC AAG GGC TAT GCT																			1470
Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala																			
50																			
55																			
60																			
GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC CCA CTC AAC GCA CAC ATG																			1518
Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met																			
65																			
70																			
75																			
AAT GCA ACC AAC CAC GCG ATT GTG CAG ACC TTG GTT CAC CTT ATG AAC																			1566
Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Leu Met Asn																			
80																			
85																			
90																			
95																			
CCC GAG TAT GTC CCC AAA CCG TGC TGT GCG CCA ACT AAG CTA AAT GCC																			1614
Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala																			
100																			
105																			
110																			
ATC TCG GTT CTT TAC TTT GAT GAC AAC TCC AAT GTC ATT CTG AAA AAA																			1662
Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys																			
115																			
120																			
125																			
TAC AGG AAT ATG GTT GTA AGA GCT TGT GGA TGC CAC TAACTCGAAA																			1708

105

Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 130 135 140

CCAGATGCTG GGGACACACA TTCTGCCTTG GATTCCTAGA TTACATCTGC CTTAAAAAAA	1768
CACGGAAGCA CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT	1828
TATTACCCAG GAAGATTTTA AAGGACCTCA TTAATAATTT GCTCACTTGG TAAATGACGT	1888
GAGTAGTTGT TGGTCTGTAG CAAGCTGAGT TTGGATGTCT GTAGCATAAG GTCTGGTAAC	1948
TGCAGAAACA TAACCGTGAA GCTCTTCCTA CCCTCCTCCC CAAAAACCC ACCAAAATTA	2008
GTTTTAGCTG TAGATCAAGC TATTTGGGGT GTTTGTTAGT AAATAGGGAA AATAATCTCA	2068
AAGGAGTTAA ATGTATTCTT GGCTAAAGGA TCAGCTGGTT CAGTACTGTC TATCAAAGGT	2128
AGATTTTACA GAGAACAGAA ATCGGGGAAG TGGGGGGAAC GCCTCTGTTC AGTTCATTCC	2188
CAGAAGTCCA CAGGACGCAC AGCCCAGGCC ACAGCCAGGG CTCCACGGGG CGCCCTTGTC	2248
TCAGTCATTG CTGTTGTATG TTCGTGCTGG AGTTTTGTTG GTGTGAAAAT ACACTTATTT	2308
CAGCCAAAAC ATACCATTTC TACACCTCAA TCCTCCATTT GCTGTACTCT TTGCTAGTAC	2368
CAAAAGTAGA CTGATTACAC TGAGGTGAGG CTACAAGGGG TGTGTAACCG TGTAACACGT	2428
GAAGGCAGTG CTCACCTCTT CTTTACCAGA ACGGTTCTTT GACCAGCACA TTAACTTCTG	2488
GACTGCCGGC TCTAGTACCT TTTCAGTAAA GTGGTTCTCT GCCTTTTTTAC TATACAGCAT	2548
ACCACGCCAC AGGGTTAGAA CCAACGAAGA AAATAAAATG AGGGTGCCCA GCTTATAAGA	2608
ATGGTGTTAG GGGGATGAGC ATGCTGTTTA TGAACGGAAA TCATGATTC CCTGTAGAAA	2668
GTGAGGCTCA GATTAAATTT TAGAATATTT TCTAAATGTC TTTTTCACAA TCATGTGACT	2728
GGGAAGGCAA TTTCATACTA AACTGATTAA ATAATACATT TATAATCTAC AACTGTTTGC	2788
ACTTACAGCT TTTTTTGTA ATATAAACTA TAATTTATTG TCTATTTTAT ATCTGTTTTG	2848
CTGTGGCGTT GGGGGGGGGG CCGGGCTTTT GGGGGGGGGG GTTTGTTTGG GGGGTGTCGT	2908
GGTGTGGGCG GCGCG	2923

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys Trp Trp Trp Gly
 -374 -370 -365 -360

106

Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu Arg Pro Pro Leu Pro
 -355 -350 -345
 Ala Ala Ala Ala Ala Ala Ala Gly Gly Gln Leu Leu Gly Asp Gly Gly
 -340 -335 -330
 Ser Pro Gly Arg Thr Glu Gln Pro Pro Pro Ser Pro Gln Ser Ser Ser
 -325 -320 -315
 Gly Phe Leu Tyr Arg Arg Leu Lys Thr Gln Glu Lys Arg Glu Met Gln
 -310 -305 -300 -295
 Lys Glu Ile Leu Ser Val Leu Gly Leu Pro His Arg Pro Arg Pro Leu
 -290 -285 -280
 His Gly Leu Gln Gln Pro Gln Pro Pro Ala Leu Arg Gln Gln Glu Glu
 -275 -270 -265
 Gln Gln Gln Gln Gln Gln Leu Pro Arg Gly Glu Pro Pro Pro Gly Arg
 -260 -255 -250
 Leu Lys Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Leu Ser
 -245 -240 -235
 Ala Asp Asn Asp Glu Asp Gly Ala Ser Glu Gly Glu Arg Gln Gln Ser
 -230 -225 -220 -215
 Trp Pro His Glu Ala Ala Ser Ser Ser Gln Arg Arg Gln Pro Pro Pro
 -210 -205 -200
 Gly Ala Ala His Pro Leu Asn Arg Lys Ser Leu Leu Ala Pro Gly Ser
 -195 -190 -185
 Gly Ser Gly Gly Ala Ser Pro Leu Thr Ser Ala Gln Asp Ser Ala Phe
 -180 -175 -170
 Leu Asn Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu Tyr
 -165 -160 -155
 Asp Lys Glu Phe Ser Pro Arg Gln Arg His His Lys Glu Phe Lys Phe
 -150 -145 -140 -135
 Asn Leu Ser Gln Ile Pro Glu Gly Glu Val Val Thr Ala Ala Glu Phe
 -130 -125 -120
 Arg Ile Tyr Lys Asp Cys Val Met Gly Ser Phe Lys Asn Gln Thr Phe
 -115 -110 -105
 Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu His Gln His Arg Asp Ser
 -100 -95 -90
 Asp Leu Phe Leu Leu Asp Thr Arg Val Val Trp Ala Ser Glu Glu Gly
 -85 -80 -75
 Trp Leu Glu Phe Asp Ile Thr Ala Thr Ser Asn Leu Trp Val Val Thr
 -70 -65 -60 -55
 Pro Gln His Asn Met Gly Leu Gln Leu Ser Val Val Thr Arg Asp Gly
 -50 -45 -40

107

Val His Val His Pro Arg Ala Ala Gly Leu Val Gly Arg Asp Gly Pro
 -35 -30 -25
 Tyr Asp Lys Gln Pro Phe Met Val Ala Phe Phe Lys Val Ser Glu Val
 -20 -15 -10
 His Val Arg Thr Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser
 -5 1 5 10
 Arg Asn Arg Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala
 15 20 25
 Ser Asp Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu
 30 35 40
 Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
 45 50 55
 Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe Pro
 60 65 70
 Leu Asn Ala His Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu
 75 80 85 90
 Val His Leu Met Asn Pro Glu Tyr Val Pro Lys Pro Cys Cys Ala Pro
 95 100 105
 Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Asn Ser Asn
 110 115 120
 Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys
 125 130 135
 His

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (H) CELL LINE: U2-OS osteosarcoma

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U2-OS human osteosarcoma cDNA library
- (B) CLONE: U2-16

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 699..2063

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1647..2060

(ix) FEATURE:

(A) NAME/KEY: mRNA

(B) LOCATION: 1..2153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGTATATT TGTGCCTGCT GGAGGTGGAA TTAACAGTAA GAAGGAGAAA GGGATTGAAT	60
GGACTTACAG GAAGGATTTC AAGTAAATTC AGGGAAACAC ATTTACTTGA ATAGTACAAC	120
CTAGAGTATT ATTTTACACT AAGACGACAC AAAAGATGTT AAAGTTATCA CCAAGCTGCC	180
GGACAGATAT ATATTCCAAC ACCAAGGTGC AGATCAGCAT AGATCTGTGA TTCAGAAATC	240
AGGATTTGTT TTGGAAAGAG CTCAAGGGTT GAGAAGAACT CAAAAGCAAG TGAAGATTAC	300
TTTGGGAACT ACAGTTTATC AGAAGATCAA CTTTGTCTAA TTCAAATACC AAAGGCCTGA	360
TTATCATAAA TTCATATAGG AATGCATAGG TCATCTGATC AAATAATATT AGCCGTCTTC	420
TGCTACATCA ATGCAGCAAA AACTCTTAAC AACTGTGGAT AATTGGAAAT CTGAGTTTCA	480
GCTTTCTTAG AAATAACTAC TCTTGACATA TTCCAAAATA TTTAAAATAG GACAGGAAAA	540
TCGGTGAGGA TGTTGTGCTC AGAAATGTCA CTGTCATGAA AAATAGGTAA ATTTGTTTTT	600
TCAGCTACTG GGAAACTGTA CCTCCTAGAA CCTTAGGTTT TTTTTTTTTT AAGAGGACAA	660
GAAGGACTAA AAATATCAAC TTTTGCTTTT GGACAAAA ATG CAT CTG ACT GTA	713
Met His Leu Thr Val	
-316-315	
TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC TGG AGC TGC TGG GTT CTA	761
Phe Leu Leu Lys Gly Ile Val Gly Phe Leu Trp Ser Cys Trp Val Leu	
-310 -305 -300	
GTG GGT TAT GCA AAA GGA GGT TTG GGA GAC AAT CAT GTT CAC TCC AGT	809
Val Gly Tyr Ala Lys Gly Gly Leu Gly Asp Asn His Val His Ser Ser	
-295 -290 -285 -280	
TTT ATT TAT AGA AGA CTA CGG AAC CAC GAA AGA CGG GAA ATA CAA AGG	857
Phe Ile Tyr Arg Arg Leu Arg Asn His Glu Arg Arg Glu Ile Gln Arg	
-275 -270 -265	
GAA ATT CTC TCT ATC TTG GGT TTG CCT CAC AGA CCC AGA CCA TTT TCA	905
Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro Phe Ser	
-260 -255 -250	
CCT GGA AAA ATG ACC AAT CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG	953
Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala Pro Leu Phe Met Leu	
-245 -240 -235	
GAT CTC TAC AAT GCC GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA	1001

Asp	Leu	Tyr	Asn	Ala	Glu	Glu	Asn	Pro	Glu	Glu	Ser	Glu	Tyr	Ser	Val		
-230						-225					-220						
AGG	GCA	TCC	TTG	GCA	GAA	GAG	ACC	AGA	GGG	GCA	AGA	AAG	GGA	TAC	CCA	1049	
Arg	Ala	Ser	Leu	Ala	Glu	Glu	Thr	Arg	Gly	Ala	Arg	Lys	Gly	Tyr	Pro		
-215					-210				-205						-200		
GCC	TCT	CCC	AAT	GGG	TAT	CCT	CGT	CGC	ATA	CAG	TTA	TCT	CGG	ACG	ACT	1097	
Ala	Ser	Pro	Asn	Gly	Tyr	Pro	Arg	Arg	Ile	Gln	Leu	Ser	Arg	Thr	Thr		
				-195				-190						-185			
CCT	CTG	ACC	ACC	CAG	AGT	CCT	CCT	CTA	GCC	AGC	CTC	CAT	GAT	ACC	AAC	1145	
Pro	Leu	Thr	Thr	Gln	Ser	Pro	Pro	Leu	Ala	Ser	Leu	His	Asp	Thr	Asn		
			-180					-175					-170				
TTT	CTG	AAT	GAT	GCT	GAC	ATG	GTC	ATG	AGC	TTT	GTC	AAC	TTA	GTT	GAA	1193	
Phe	Leu	Asn	Asp	Ala	Asp	Met	Val	Met	Ser	Phe	Val	Asn	Leu	Val	Glu		
		-165				-160						-155					
AGA	GAC	AAG	GAT	TTT	TCT	CAC	CAG	CGA	AGG	CAT	TAC	AAA	GAA	TTT	CGA	1241	
Arg	Asp	Lys	Asp	Phe	Ser	His	Gln	Arg	Arg	His	Tyr	Lys	Glu	Phe	Arg		
-150						-145					-140						
TTT	GAT	CTT	ACC	CAA	ATT	CCT	CAT	GGA	GAG	GCA	GTG	ACA	GCA	GCT	GAA	1289	
Phe	Asp	Leu	Thr	Gln	Ile	Pro	His	Gly	Glu	Ala	Val	Thr	Ala	Ala	Glu		
-135					-130				-125						-120		
TTC	CGG	ATA	TAC	AAG	GAC	CGG	AGC	AAC	AAC	CGA	TTT	GAA	AAT	GAA	ACA	1337	
Phe	Arg	Ile	Tyr	Lys	Asp	Arg	Ser	Asn	Asn	Arg	Phe	Glu	Asn	Glu	Thr		
				-115				-110						-105			
ATT	AAG	ATT	AGC	ATA	TAT	CAA	ATC	ATC	AAG	GAA	TAC	ACA	AAT	AGG	GAT	1385	
Ile	Lys	Ile	Ser	Ile	Tyr	Gln	Ile	Ile	Lys	Glu	Tyr	Thr	Asn	Arg	Asp		
			-100					-95					-90				
GCA	GAT	CTG	TTC	TTG	TTA	GAC	ACA	AGA	AAG	GCC	CAA	GCT	TTA	GAT	GTG	1433	
Ala	Asp	Leu	Phe	Leu	Leu	Asp	Thr	Arg	Lys	Ala	Gln	Ala	Leu	Asp	Val		
		-85				-80						-75					
GGT	TGG	CTT	GTC	TTT	GAT	ATC	ACT	GTG	ACC	AGC	AAT	CAT	TGG	GTG	ATT	1481	
Gly	Trp	Leu	Val	Phe	Asp	Ile	Thr	Val	Thr	Ser	Asn	His	Trp	Val	Ile		
	-70					-65					-60						
AAT	CCC	CAG	AAT	AAT	TTG	GGC	TTA	CAG	CTC	TGT	GCA	GAA	ACA	GGG	GAT	1529	
Asn	Pro	Gln	Asn	Asn	Leu	Gly	Leu	Gln	Leu	Cys	Ala	Glu	Thr	Gly	Asp		
-55					-50					-45					-40		
GGA	CGC	AGT	ATC	AAC	GTA	AAA	TCT	GCT	GGT	CTT	GTG	GGA	AGA	CAG	GGA	1577	
Gly	Arg	Ser	Ile	Asn	Val	Lys	Ser	Ala	Gly	Leu	Val	Gly	Arg	Gln	Gly		
				-35				-30						-25			
CCT	CAG	TCA	AAA	CAA	CCA	TTC	ATG	GTG	GCC	TTC	TTC	AAG	GCG	AGT	GAG	1625	
Pro	Gln	Ser	Lys	Gln	Pro	Phe	Met	Val	Ala	Phe	Phe	Lys	Ala	Ser	Glu		
			-20					-15					-10				
GTA	CTT	CTT	CGA	TCC	GTG	AGA	GCA	GCC	AAC	AAA	CGA	AAA	AAT	CAA	AAC	1673	
Val	Leu	Leu	Arg	Ser	Val	Arg	Ala	Ala	Asn	Lys	Arg	Lys	Asn	Gln	Asn		
		-5					1				5						
CGC	AAT	AAA	TCC	AGC	TCT	CAT	CAG	GAC	TCC	TCC	AGA	ATG	TCC	AGT	GTT	1721	

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Arg	Asn	Lys	Ser	Ser	Ser	His	Gln	Asp	Ser	Ser	Arg	Met	Ser	Ser	Val	
10					15					20					25	
GGA	GAT	TAT	AAC	ACA	AGT	GAG	CAA	AAA	CAA	GCC	TGT	AAG	AAG	CAC	GAA	1769
Gly	Asp	Tyr	Asn	Thr	Ser	Glu	Gln	Lys	Gln	Ala	Cys	Lys	Lys	His	Glu	
				30					35					40		
CTC	TAT	GTG	AGC	TTC	CGG	GAT	CTG	GGA	TGG	CAG	GAC	TGG	ATT	ATA	GCA	1817
Leu	Tyr	Val	Ser	Phe	Arg	Asp	Leu	Gly	Trp	Gln	Asp	Trp	Ile	Ile	Ala	
			45					50					55			
CCA	GAA	GGA	TAC	GCT	GCA	TTT	TAT	TGT	GAT	GGA	GAA	TGT	TCT	TTT	CCA	1865
Pro	Glu	Gly	Tyr	Ala	Ala	Phe	Tyr	Cys	Asp	Gly	Glu	Cys	Ser	Phe	Pro	
		60					65					70				
CTT	AAC	GCC	CAT	ATG	AAT	GCC	ACC	AAC	CAC	GCT	ATA	GTT	CAG	ACT	CTG	1913
Leu	Asn	Ala	His	Met	Asn	Ala	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	
	75					80					85					
GTT	CAT	CTG	ATG	TTT	CCT	GAC	CAC	GTA	CCA	AAG	CCT	TGT	TGT	GCT	CCA	1961
Val	His	Leu	Met	Phe	Pro	Asp	His	Val	Pro	Lys	Pro	Cys	Cys	Ala	Pro	
	90				95				100						105	
ACC	AAA	TTA	AAT	GCC	ATC	TCT	GTT	CTG	TAC	TTT	GAT	GAC	AGC	TCC	AAT	2009
Thr	Lys	Leu	Asn	Ala	Ile	Ser	Val	Leu	Tyr	Phe	Asp	Asp	Ser	Ser	Asn	
			110						115					120		
GTC	ATT	TTG	AAA	AAA	TAT	AGA	AAT	ATG	GTA	GTA	CGC	TCA	TGT	GGC	TGC	2057
Val	Ile	Leu	Lys	Lys	Tyr	Arg	Asn	Met	Val	Val	Arg	Ser	Cys	Gly	Cys	
			125					130					135			
CAC	TAATATTAAA	TAATATTGAT	AATAACAAAA	AGATCTGTAT	TAAGGTTTAT											2110
His																
GGCTGCAATA	AAAAGCATAC	TTTCAGACAA	ACAGAAAAAA	AAA												2153

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	His	Leu	Thr	Val	Phe	Leu	Leu	Lys	Gly	Ile	Val	Gly	Phe	Leu	Trp	
-316	-315						-310				-305					
Ser	Cys	Trp	Val	Leu	Val	Gly	Tyr	Ala	Lys	Gly	Gly	Leu	Gly	Asp	Asn	
-300				-295						-290					-285	
His	Val	His	Ser	Ser	Phe	Ile	Tyr	Arg	Arg	Leu	Arg	Asn	His	Glu	Arg	
			-280					-275					-270			
Arg	Glu	Ile	Gln	Arg	Glu	Ile	Leu	Ser	Ile	Leu	Gly	Leu	Pro	His	Arg	
			-265				-260						-255			

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Pro Arg Pro Phe Ser Pro Gly Lys Met Thr Asn Gln Ala Ser Ser Ala
 -250 -245 -240
 Pro Leu Phe Met Leu Asp Leu Tyr Asn Ala Glu Glu Asn Pro Glu Glu
 -235 -230 -225
 Ser Glu Tyr Ser Val Arg Ala Ser Leu Ala Glu Glu Thr Arg Gly Ala
 -220 -215 -210 -205
 Arg Lys Gly Tyr Pro Ala Ser Pro Asn Gly Tyr Pro Arg Arg Ile Gln
 -200 -195 -190
 Leu Ser Arg Thr Thr Pro Leu Thr Thr Gln Ser Pro Pro Leu Ala Ser
 -185 -180 -175
 Leu His Asp Thr Asn Phe Leu Asn Asp Ala Asp Met Val Met Ser Phe
 -170 -165 -160
 Val Asn Leu Val Glu Arg Asp Lys Asp Phe Ser His Gln Arg Arg His
 -155 -150 -145
 Tyr Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala
 -140 -135 -130 -125
 Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg
 -120 -115 -110
 Phe Glu Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu
 -105 -100 -95
 Tyr Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala
 -90 -85 -80
 Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr Ser
 -75 -70 -65
 Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln Leu Cys
 -60 -55 -50 -45
 Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser Ala Gly Leu
 -40 -35 -30
 Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe Met Val Ala Phe
 -25 -20 -15
 Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val Arg Ala Ala Asn Lys
 -10 -5 1
 Arg Lys Asn Gln Asn Arg Asn Lys Ser Ser Ser His Gln Asp Ser Ser
 5 10 15 20
 Arg Met Ser Ser Val Gly Asp Tyr Asn Thr Ser Glu Gln Lys Gln Ala
 25 30 35
 Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln
 40 45 50
 Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Phe Tyr Cys Asp Gly
 55 60 65

Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala Thr Asn His Ala
 70 75 80
 Ile Val Gln Thr Leu Val His Leu Met Phe Pro Asp His Val Pro Lys
 85 90 95 100
 Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe
 105 110 115
 Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn Met Val Val
 120 125 130
 Arg Ser Cys Gly Cys His
 135

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens
- (F) TISSUE TYPE: Human Heart

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human heart cDNA library stratagene catalog
#936208
- (B) CLONE: hH38

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8..850

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 427..843

(ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 1..997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC
 Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile
 -139 -135 -130

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CCG GCT GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG Pro Ala Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val -125 -120 -115 -110	9:
CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG Pro Ser Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln -105 -100 -95	14:
GTG GTC CAG GAG CAG TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT Val Val Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp -90 -85 -80	19:
CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG CTG GTG CTG GAT GTC Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val -75 -70 -65	24:
ACA GCA GCC AGT GAC TGC TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA Thr Ala Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly -60 -55 -50	28:
CTC CGC CTC TAT GTG GAG ACT GAG GAT GGG CAC AGC GTG GAT CCT GGC Leu Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly -45 -40 -35 -30	33:
CTG GCC GGC CTG CTG GGT CAA CGG GCC CCA CGC TCC CAA CAG CCT TTC Leu Ala Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe -25 -20 -15	38:
GTG GTC ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG Val Val Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg -10 -5 1	43:
GCA GTG AGG CCA CTG AGG AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu 5 10 15	48:
CCG CAG GCC AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser 20 25 30 35	52:
CAC GGC CGG CAG GTC TGC CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln 40 45 50	57:
GAC CTT GGC TGG CTG GAC TGG GTC ATC GCC CCC CAA GGC TAC TCA GCC Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala 55 60 65	62:
TAT TAC TGT GAG GGG GAG TGC TCC TTC CCG CTG GAC TCC TGC ATG AAC Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn 70 75 80	67:
GCC ACC AAC CAC GCC ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro 85 90 95	72:
AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG CTG AGC GCC ACC Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr 100 105 110 115	76:

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TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC	817
Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His	
120 125 130	
CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCC CGCCCAGCCC	870
Arg Asn Met Val Val Lys Ala Cys Gly Cys His	
135 140	
TACTGCAGCC ACCCTTCTCA TCTGGATCGG GCCCTGCAGA GGCAGAAAAC CCTTAAATGC	930
TGTCACAGCT CAAGCAGGAG TGTCAGGGGC CCTCACTCTC GGTGCCTACT TCCTGTCAGG	990
CTTCTGGGAA TTC	1003

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala	-125
-139 -135 -130	
Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser	-110
-120 -115	
Ile His Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val	-95
-105 -100	
Gln Glu Gln Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln	-80
-90 -85	
Thr Leu Arg Ala Gly Asp Glu Gly Trp Leu Val Leu Asp Val Thr Ala	-60
-75 -70 -65	
Ala Ser Asp Cys Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu Arg	-45
-55 -50	
Leu Tyr Val Glu Thr Glu Asp Gly His Ser Val Asp Pro Gly Leu Ala	-30
-40 -35	
Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val	-15
-25 -20	
Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg Ala Val	5
-10 -5 1	
Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln	20
10 15	
Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly	35
25 30	
Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu	

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Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr
 55 60 65
 Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr
 70 75 80 85
 Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro Asn Ala
 90 95 100
 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
 105 110 115
 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
 120 125 130
 Met Val Val Lys Ala Cys Gly Cys His
 135 140

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2623 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: pALBP2-781

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2724..3071

(ix) FEATURE:

- (A) NAME/KEY: terminator
- (B) LOCATION: 3150..3218

(ix) FEATURE:

- (A) NAME/KEY: RBS
- (B) LOCATION: 2222..2723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTAA TGTCATGATA ATAATGGTTT 60
 CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCCTATT TGTTTATTTT 120
 TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACCCTGATAA ATGCTTCAAT 180
 AATATTGAAA AAGGAAGAGT ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCTTTT 240
 TTGCGGCATT TTGCCTTCCT GTTTTGTCTC ACCCAGAAAC GCTGGTGAAG GTAAAAGATG 300
 CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA 360

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TCCTTGAGAG	TTTTCGCCCC	GAAGAACGTT	TTCCAATGAT	GAGCACTTTT	AAAGTTCTGC	420
TATGTGGCGC	GGTATTATCC	CGTATTGACG	CCGGGCAAGA	GCAACTCGGT	CGCCGCATAC	480
ACTATTCTCA	GAATGACTTG	GTTGAGTACT	CACCAGTCAC	AGAAAAGCAT	CTTACGGATG	540
GCATGACAGT	AAGAGAATTA	TGCAGTGCTG	CCATAACCAT	GAGTGATAAC	ACTGCGGCCA	600
ACTTACTTCT	GACAACGATC	GGAGGACCGA	AGGAGCTAAC	CGCTTTTTTG	CACAACATGG	660
GGGATCATGT	AACTCGCCTT	GATCGTTGGG	AACCGGAGCT	GAATGAAGCC	ATACCAAACG	720
ACGAGCGTGA	CACCACGATG	CCTGTAGCAA	TGGCAACAAC	GTTGCGCAAA	CTATTAAGTG	780
GCGAACTACT	TACTCTAGCT	TCCCGGCAAC	AATTAATAGA	CTGGATGGAG	GCGGATAAAG	840
TTGCAGGACC	ACTTCTGCGC	TCGGCCCTTC	CGGCTGGCTG	GTTTATTGCT	GATAAATCTG	900
GAGCCGGTGA	GCGTGGGTCT	CGCGGTATCA	TTGCAGCACT	GGGGCCAGAT	GGTAAGCCCT	960
CCCGTATCGT	AGTTATCTAC	ACGACGGGGA	GTCAGGCAAC	TATGGATGAA	CGAAATAGAC	1020
AGATCGCTGA	GATAGGTGCC	TCACTGATTA	AGCATTGGTA	ACTGTCAGAC	CAAGTTTACT	1080
CATATATACT	TTAGATTGAT	TTAAAACTTC	ATTTTAAATT	TAAAAGGATC	TAGGTGAAGA	1140
TCCTTTTTGA	TAATCTCATG	ACCAAAATCC	CTTAACGTGA	GTTTTTCGTT	CACTGAGCGT	1200
CAGACCCCGT	AGAAAAGATC	AAAGGATCTT	CTTGAGATCC	TTTTTTTCTG	CGCGTAATCT	1260
GCTGCTTGCA	AACAAAAAAA	CCACCGCTAC	CAGCGGTGGT	TTGTTTGCCG	GATCAAGAGC	1320
TACCAACTCT	TTTTCCGAAG	GTAAGTGGCT	TCAGCAGAGC	GCAGATACCA	AATACTGTCC	1380
TTCTAGTGTA	GCCGTAGTTA	GGCCACCACT	TCAAGAACTC	TGTAGCACCG	CCTACATACC	1440
TCGCTCTGCT	AATCCTGTTA	CCAGTGGCTG	CTGCCAGTGG	CGATAAGTCG	TGTCTTACCG	1500
GGTTGGACTC	AAGACGATAG	TTACCGGATA	AGGCGCAGCG	GTCGGGCTGA	ACGGGGGGTT	1560
CGTGACACAC	GCCCAGCTTG	GAGCGAACGA	CCTACACCGA	ACTGAGATAC	CTACAGCGTG	1620
AGCATTGAGA	AAGCGCCACG	CTTCCCGAAG	GGAGAAAGGC	GGACAGGTAT	CCGGTAAGCG	1680
GCAGGGTCGG	AACAGGAGAG	CGCACGAGGG	AGCTTCCAGG	GGGAAACGCC	TGGTATCTTT	1740
ATAGTCCTGT	CGGGTTTCGC	CACCTCTGAC	TTGAGCGTCG	ATTTTTGTGA	TGCTCGTCAG	1800
GGGGGCGGAG	CCTATGGAAA	AACGCCAGCA	ACGCGGCCTT	TTTACGGTTC	CTGGCCTTTT	1860
GCTGGCCTTT	TGCTCACATG	TTCTTTCTCG	CGTTATCCCC	TGATTCTGTG	GATAACCGTA	1920
TTACCGCCTT	TGAGTGAGCT	GATACCGCTC	GCCGCAGCCG	AACGACCGAG	CGCAGCGAGT	1980
CAGTGAGCGA	GGAAGCGGAA	GAGCGCCCAA	TACGCAAACC	GCCTCTCCCC	GCGCGTTGGC	2040
CGATTCATTA	ATGCAGAATT	GATCTCTCAC	CTACCAAACA	ATGCCCCCCT	GCAAAAAATA	2100
AATTCATATA	AAAAACATAC	AGATAACCAT	CTGCGGTGAT	AAATTATCTC	TGGCGGTGTT	2160

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GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GGACGCACTG ACCACCATGA	2220
AGGTGACGCT CTTAAAAATT AAGCCCTGAA GAAGGGCAGC ATTCAAAGCA GAAGGCTTTG	2280
GGGTGTGTGA TACGAAACGA AGCATTGGCC GTAAGTGCGA TTCCGGATTA GCTGCCAATG	2340
TGCCAATCGC GGGGGGTTTT CGTTCAGGAC TACAACCTGCC ACACACCACC AAAGCTAACT	2400
GACAGGAGAA TCCAGATGGA TGCACAAACA CGCCGCCGCG AACGTCGCGC AGAGAAACAG	2460
GCTCAATGGA AAGCAGCAAA TCCCCTGTTG GTTGGGGTAA GCGCAAAACC AGTTCCGAAA	2520
GATTTTTTTTA ACTATAAACG CTGATGGAAG CGTTTATGCG GAAGAGGTAA AGCCCTTCCC	2580
GAGTAACAAA AAAACAACAG CATAAATAAC CCCGCTCTTA CACATTCCAG CCCTGAAAAA	2640
GGGCATCAAA TTAAACCACA CCTATGGTGT ATGCATTTAT TTGCATACAT TCAATCAATT	2700
GTTATCTAAG GAAATACTTA CAT ATG CAA GCT AAA CAT AAA CAA CGT AAA	2750
Met Gln Ala Lys His Lys Gln Arg Lys	
1 5	
CGT CTG AAA TCT AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC TTC AGT	2798
Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp Phe Ser	
10 15 20 25	
GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC	2846
Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala	
30 35 40	
TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC	2894
Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn	
45 50 55	
TCC ACT AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT	2942
Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser	
60 65 70	
AAG ATT CCT AAG GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG	2990
Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser	
75 80 85	
ATG CTG TAC CTT GAC GAG AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG	3038
Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn Tyr Gln	
90 95 100 105	
GAC ATG GTT GTG GAG GGT TGT GGG TGT CGC TAGTACAGCA AAATTAAATA	3088
Asp Met Val Val Glu Gly Cys Gly Cys Arg	
110 115	
CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA AAAATCTAGA GTCGACCTGC	3148
AGTAATCGTA CAGGGTAGTA CAAATAAAAA AGGCACGTCA GATGACGTGC CTTTTTTCTT	3208
GTGAGCAGTA AGCTTGGCAC TGGCCGTCGT TTTACAACGT CGTGACTGGG AAAACCCTGG	3268
CGTTACCCAA CTTAATCGCC TTGCAGCACA TCCCCCTTTC GCCAGCTGGC GTAATAGCGA	3328
AGAGGCCCGC ACCGATCGCC CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGCGCCT	3388

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GATGCGGTAT TTTCTCCTTA CGCATCTGTG CGGTATTTCA CACCGCATAT ATGGTGCACT 3448
 CTCAGTACAA TCTGCTCTGA TGCCGCATAG TTAAGCCAGC CCCGACACCC GCCAACACCC 3508
 GCTGACGCGC CCTGACGGGC TTGTCTGCTC CCGGCATCCG CTTACAGACA AGCTGTGACC 3568
 GTCTCCGGGA GCTGCATGTG TCAGAGGTTT TCACCGTCAT CACCGAAACG CGCGA 3623

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys
 1 5 10 15
 Arg His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp
 20 25 30
 Ile Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys
 35 40 45
 Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val
 50 55 60
 Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys
 65 70 75 80
 Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn
 85 90 95
 Glu Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys
 100 105 110
 Gly Cys Arg
 115

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CATGGGCAGC TGAG

14

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAGGGTTGTG GGTGTCGCTA GTGAGTCGAC TACAGCAAAT T

41

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGATGTGGGT GCCGCTGACT CTAGAGTCGA CGGAATTC

38

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATTCACCAT GATTCCTGGT AACCGAATGC T

31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGGTACTAA GGACCATTTGG CTTAC

25

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGACCTGCAG CCATGCATCT GACTGTA

27

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGCCTGCAGT TTAATATTAG TGGCAGC

27

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGACCTGCAG CCACC

15

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCGACCCACC ATGCCGGGGC TGGGGCGGAG GCGCAGTGG CTGTGCTGGT GGTGGGGGCT 60

GTGCTGCAGC TGCTGCGGGC C 81

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCAGCAGCT GCACAGCAGC CCCCACCACC AGCACAGCCA CTGCGCCCTC CGCCCCAGCC 60

CCGGCATGGT GGG 73

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCGACTGGTT T 11

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGAAACCAG

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(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCGACAGGCT CGCCTGCA

18

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCCGAGCGG

10

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTCGACC CACCATGCAC GTGCGCTCA

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TCTGTCGACC TCGGAGGAGC TAGTGGC

27

WHAT IS CLAIMED IS:

1. A method for producing a heterodimeric protein having bone stimulating activity comprising culturing a selected host cell containing a sequence encoding a first selected BMP or fragment thereof and a sequence encoding a second selected BMP or fragment thereof, said sequences each being under the control of a suitable regulatory sequence capable of directing co-expression of said proteins, and isolating said heterodimeric protein from the culture medium.

2. The method according to claim 1 wherein said first BMP or fragment thereof is present on a first vector transfected into said host cell and said second BMP or fragment thereof is present on a second vector transfected into said host cell.

3. The method according to claim 1 wherein both said BMPs or fragments thereof are incorporated into a chromosome of said host cell.

4. The method according to claim 1 wherein both BMPs or fragments thereof are present on a single vector.

5. The method according to claim 2 wherein

more than a single copy of the gene encoding each said BMP or fragment thereof is present on each vector.

6. The method according to claim 1 wherein said host cell is a hybrid cell prepared by culturing two fused selected, stable host cells, each host cell transfected with a sequence encoding a selected first or second BMP or fragment thereof, said sequences under the control of a suitable regulatory sequence capable of directing expression of each protein or fragment.

7. The method according to claim 1 wherein said host cell is a mammalian cell.

8. The method according to claim 1 wherein said host cell is an insect cell.

9. The method according to claim 1 wherein said host cell is a yeast cell.

10. A method for producing a heterodimeric protein having bone stimulating activity in a bacterial cell comprising culturing a selected host cell containing a sequence encoding a first selected BMP or fragment thereof under the control of a suitable regulatory sequence capable of directing expression of the protein or protein fragment under conditions suitable for the

formation of a soluble, monomeric protein; culturing a
selected host cell containing a sequence encoding a
second selected BMP or fragment thereof under the control
of a suitable regulatory sequence capable of directing
5 expression of the protein or protein fragment under said
conditions to form a second soluble, monomeric protein;
and mixing said soluble monomeric proteins under
conditions permitting the formation of dimeric proteins
associated by at least one covalent disulfide bond;
10 isolating from the mixture a heterodimeric protein.

11. The method according to claim 10 wherein
said host cell is *E. coli*.

12. The method according to claim 10 wherein
said conditions comprise treating said protein with a
15 solubilizing agent.

13. A recombinant heterodimeric protein having
bone stimulating activity comprising a first protein or
fragment of BMP-2 in association with a second protein or
fragment thereof selected from the group consisting of
20 BMP-5, BMP-6, BMP-7 and BMP-8.

14. The protein according to claim 13 wherein
said second protein is BMP-5.

15. The protein according to claim 13 wherein said second protein is BMP-6.

16. The protein according to claim 13 wherein said second protein is BMP-7.

5 17. The protein according to claim 13 wherein said second protein is BMP-8.

18. A recombinant heterodimeric protein having bone stimulating activity comprising a protein or fragment of BMP-4 in association with a second protein or
10 fragment thereof selected from the group consisting of BMP-5, BMP-6, BMP-7 and BMP-8.

19. The protein according to claim 18 wherein said second protein is BMP-5.

20. The protein according to claim 18 wherein
15 said second protein is BMP-6.

21. The protein according to claim 18 wherein said second protein is BMP-7.

22. The protein according to claim 18 wherein said second protein is BMP-8.

23. A recombinant heterodimeric protein having bone stimulating activity comprising a protein or fragment of a first BMP in association with a second protein or fragment of a second BMP produced by co-expressing said proteins in a selected host cell.

24. The protein according to claim 23 wherein said first BMP is BMP-2 and said second BMP is BMP-7.

25. A cell line comprising a nucleotide sequence encoding a first BMP or fragment thereof under control of a suitable expression regulatory system and a nucleotide sequence encoding a second BMP or fragment thereof under control of a suitable expression regulatory system, said regulatory systems capable of directing the co-expression of said BMPs or fragments thereof and the formation of heterodimeric protein.

26. The cell line according to claim 25 wherein said nucleotide sequences encoding said first and second BMP proteins are present in a single DNA molecule.

27. The cell line according to claim 25 wherein said nucleotide sequence encoding said first BMP is present on a first DNA molecule and said nucleotide sequence encoding said second BMP is present on a second DNA molecule.

28. The cell line according to claim 26
wherein said single DNA molecule comprises a first
transcription unit containing a gene encoding a first BMP
or fragment thereof and a second transcription unit
5 containing a gene encoding a second BMP or fragment
thereof.

29. The cell line according to claim 26
wherein said single DNA molecule comprises a single
transcription unit containing multiple copies of said
10 gene encoding said first BMP or fragments thereof and
multiple copies of said gene encoding said second BMP or
fragments thereof.

30. A DNA molecule comprising a sequence
encoding a first selected BMP or fragment thereof and a
15 sequence encoding a second selected BMP or fragment
thereof, said sequences under the control of at least one
suitable regulatory sequence capable of directing co-
expression of each BMP or fragment thereof.

31. The molecule according to claim 30
20 comprising a first transcription unit containing a gene
encoding a first BMP or fragment thereof and a second
transcription unit containing a gene encoding a second
BMP or fragment thereof.

32. The molecule according to claim 30 comprising a single transcription unit containing multiple copies of said gene encoding said first BMP or fragments thereof and multiple copies of said gene encoding said second BMP or fragments thereof.

33. The protein according to claim 23 wherein said first BMP is BMP-2 and said second BMP is BMP-6.

34. A recombinant BMP-2 homodimer having bone stimulating activity said homodimer produced in E. coli.

35. A method for producing a homodimeric BMP-2 protein having bone stimulating activity said method comprising culturing E. coli host cells and isolating and purifying said protein from the resulting culture medium.

36. A recombinant heterodimeric protein having bone stimulating activity comprising a first protein or fragment of BMP-2 in association with a second protein or fragment of BMP-2.

FIGURE 1A

10 20 30 40 50 60 70
 GTCGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT AACTTGCGCA
 80 90 100 110 120 130 140
 CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT CCGAGCCCCA CCGCCCCCTCC
 150 160 170 180 190 200 210
 ACTCCTCGGC CTTGCCCCGAC ACTGAGACGC TGTTCCTCAGC GTGAAAAGAG AGACTGCGCG GCCGGCACCC
 220 230 240 250 260 270 280
 GGGAGAAGGA GGAGGCAAAG AAAAGGAACG GACATTCGGT CCTTGCGCCA GGTCCTTTGA CCAGAGTTTT
 290 300 310 320 330 340 350
 TCCATGTGGA CGCTCTTTCA ATGGACGTGT CCCC GCGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT
 (1) 370 385 400
 CGACC ATG GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC
 MET Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val
 415 430 445
 CTC CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC GCG
 Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe Ala
 (24)
 460 475 490 505
 GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC CTG AGC GAG
 Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val Leu Ser Glu
 520 535 550 565
 TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG AGA CCC ACC CCC AGC
 Phe Glu Leu Arg Leu Leu Ser MET Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser
 580 595 610
 AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC CTG TAT CGC AGG CAC TCA GGT
 Arg Asp Ala Val Val Pro Pro Tyr MET Leu Asp Leu Tyr Arg Arg His Ser Gly
 625 640 655 670
 CAG CCG GGC TCA CCC GCC CCA GAC CAC CGG TTG GAG AGG GCA GCC AGC CGA GCC
 Gln Pro Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala

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FIGURE 1B

685 700 715
 AAC ACT GTG CGC AGC TTC CAC CAT GAA GAA TCT TTG GAA GAA CTA CCA GAA ACG
 Asn Thr Val Arg Ser Phe His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr
 730 745 760 775
 AGT GGG AAA ACA ACC CGG AGA TTC TTC TTT AAT TTA AGT TCT ATC CCC ACG GAG
 Ser Gly Lys Thr Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu
 790 805 820 835
 GAG TTT ATC ACC TCA GCA GAG CTT CAG GTT TTC CGA GAA CAG ATG CAA GAT GCT
 Glu Phe Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln MET Gln Asp Ala
 850 865 880
 TTA GGA AAC AAT AGC AGT TTC CAT CAC CGA ATT AAT ATT TAT GAA ATC ATA AAA
 Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile Lys
 895 910 925 940
 CCT GCA ACA GCC AAC TCG AAA TTC CCC GTG ACC AGA CTT TTG GAC ACC AGG TTG
 Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu Asp Thr Arg Leu
 955 970 985
 GTG AAT CAG AAT GCA AGC AGG TGG GAA AGT TTT GAT GTC ACC CCC GCT GTG ATG
 Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp Val Thr Pro Ala Val MET
 1000 1015 1030 1045
 CGG TGG ACT GCA CAG GGA CAC GCC AAC CAT GGA TTC GTG GTG GAA GTG GCC CAC
 Arg Trp Thr Ala Gln Gly His Ala Asn His Gly Phe Val Val Glu Val Ala His
 1060 1075 1090 1105
 TTG GAG GAG AAA CAA GGT GTC TCC AAG AGA CAT GTT AGG ATA AGC AGG TCT TTG
 Leu Glu Glu Lys Gln Gly Val Ser Lys Arg His Val Arg Ile Ser Arg Ser Leu
 (249)
 1120 1135 1150
 CAC CAA GAT GAA CAC AGC TGG TCA CAG ATA AGG CCA TTG CTA GTA ACT TTT GGC
 His Gln Asp Glu His Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly
 (266)
 1165 1180 1195 1210
 CAT GAT GGA AAA GGG CAT CCT CTC CAC AAA AGA GAA AAA CGT CAA GCC AAA CAC
 His Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His
 (283)
 1225 1240 1255
 AAA CAG CGG AAA CGC CTT AAG TCC AGC TGT AAG AGA CAC CCT TTG TAC GTG GAC
 Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
 (296)
 1270 1285 1300 1315
 TTC AGT GAC GTG GGG TGG AAT GAC TGG ATT GTG GCT CCC CCG GGG TAT CAC GCC
 Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr His Ala

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FIGURE 1C

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      1330      1345      1360      1375
TTT TAC TGC CAC GGA GAA TGC CCT TTT CCT CTG GCT GAT CAT CTG AAC TCC ACT
Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
      1390      1405      1420
AAT CAT GCC ATT GTT CAG ACG TTG GTC AAC TCT GTT AAC TCT AAG ATT CCT AAG
Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys

      1435      1450      1465      1480
GCA TGC TGT GTC CCG ACA GAA CTC AGT GCT ATC TCG ATG CTG TAC CTT GAC GAG
Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser MET Leu Tyr Leu Asp Glu

      1495      1510      1525
AAT GAA AAG GTT GTA TTA AAG AAC TAT CAG GAC ATG GTT GTG GAG GGT TGT GGG
Asn Glu Lys Val Val Leu Lys Asn Tyr Gln Asp MET Val Val Glu Gly Cys Gly

1540(396)      1553      1563      1573      1583      1593      1603
TGT CGC TAGTACAGCA AAATTAAATA CATAAATATA TATATATATA TATATTTTAG AAAAAAGAAA
Cys Arg

```

AAAA

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FIGURE 2A

10 20 30 40 50 60 70
 CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCCGGC CCGGAAGCTA GGTGAGTGTG
 80 90 100 110 120 130 140
 GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG AGTATCTAGC TTGTCTCCCC
 150 160 170 180 190 200 210
 GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC ACAGTCCCCG GCCCTCGCCC AGGTTCACTG
 220 230 240 250 260 270 280
 CAACCGTTCA GAGGTCCCCA GGAGCTGCTG CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC
 290 300 310 320 330 340 350
 GTAGTGCCAT CCCGAGCAAC GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG
 360 370 380 390 400 (1)
 CTGTCAAGAA TCATGGACTG TTATTATATG CCTTGTTTTT TGTCAAGACA CC ATG ATT CCT
 MET Ile Pro
 417 432 447 462
 GGT AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC GCG
 Gly Asn Arg MET Leu MET Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly Ala
 477 492 507
 AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC GAG ATT CAG
 Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala Glu Ile Gln
 522 537 552 567
 GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG CTC CTG CGG GAC TTC
 Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu Leu Leu Arg Asp Phe
 582 597 612 627
 GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC CGC CCG CAG CCT AGC AAG
 Glu Ala Thr Leu Leu Gln MET Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys
 642 657 672
 AGT GCC GTC ATT CCG GAC TAC ATG CGG GAT CTT TAC CGG CTT CAG TCT GGG GAG
 Ser Ala Val Ile Pro Asp Tyr MET Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu

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FIGURE 2B

687 702 717 732
 GAG GAG GAA GAG CAG ATC CAC AGC ACT GGT CTT GAG TAT CCT GAG CGC CCG GCC
 Glu Glu Glu Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala

747 762 777
 AGC CGG GCC AAC ACC GTG AGG AGC TTC CAC CAC GAA GAA CAT CTG GAG AAC ATC
 Ser Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn Ile

792 807 822 837
 CCA GGG ACC AGT GAA AAC TCT GCT TTT CGT TTC CTC TTT AAC CTC AGC AGC ATC
 Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu Ser Ser Ile

852 867 882 897
 CCT GAG AAC GAG GTG ATC TCC TCT GCA GAG CTT CGG CTC TTC CGG GAG CAG GTG
 Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu Phe Arg Glu Gln Val

912 927 942
 GAC CAG GGC CCT GAT TGG GAA AGG GGC TTC CAC CGT ATA AAC ATT TAT GAG GTT
 Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His Arg Ile Asn Ile Tyr Glu Val

957 972 987 1002
 ATG AAG CCC CCA GCA GAA GTG GTG CCT GGG CAC CTC ATC ACA CGA CTA CTG GAC
 MET Lys Pro Pro Ala Glu Val Val Pro Gly His Leu Ile Thr Arg Leu Leu Asp

1017 1032 1047
 ACG AGA CTG GTC CAC CAC AAT GTG ACA CGG TGG GAA ACT TTT GAT GTG AGC CCT
 Thr Arg Leu Val His His Asn Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro

1062 1077 1092 1107
 GCG GTC CTT CGC TGG ACC CGG GAG AAG CAG CCA AAC TAT GGG CTA GCC ATT GAG
 Ala Val Leu Arg Trp Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu

1122 1137 1152 1167
 GTG ACT CAC CTC CAT CAG ACT CGG ACC CAC CAG GGC CAG CAT GTC AGG ATT AGC
 Val Thr His Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser

1182 1197 1212
 CGA TCG TTA CCT CAA GGG AGT GGG AAT TGG GCC CAG CTC CGG CCC CTC CTG GTC
 Arg Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu Val

1227 1242 1257 1272
 ACC TTT GGC CAT GAT GGC CGG GGC CAT GCC TTG ACC CGA CGC CGG AGG GCC AAG
 Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg Ala Lys

1287 1302 1317
 CGT AGC CCT AAG CAT CAC TCA CAG CGG GCC AGG AAG AAG AAT AAG AAC TGC CGG
 Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys Arg
 (293)

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FIGURE 2C

1332 1347 1362 1377
 CGC CAC TCG CTC TAT GTG GAC TTC AGC GAT GTG GGC TGG AAT GAC TGG ATT GTG
 Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val

1392 1407 1422 1437
 GCC CCA CCA GGC TAC CAG GCC TTC TAC TGC CAT GGC GAC TGC CCC TTT CCA CTG
 Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp Cys Pro Phe Pro Leu

1452 1467 1482
 GCT GAC CAC CTC AAC TCA ACC AAC CAT GCC ATT GTG CAG ACC CTG GTC AAT TCT
 Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser

1497 1512 1527 1542
 GTC AAT TCC AGT ATC CCC AAA GCC TGT TGT GTG CCC ACT GAA CTG AGT GCC ATC
 Val Asn Ser Ser Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile

1557 1572 1587
 TCC ATG CTG TAC CTG GAT GAG TAT GAT AAG GTG GTA CTG AAA AAT TAT CAG GAG
 Ser MET Leu Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu

1602 1617 (408) 1636 1646 1656
 ATG GTA GTA GAG GGA TGT GGG TGC CGC TGAGATCAGG CAGTCCTTGA GGATAGACAG
MET Val Val Glu Gly Cys Gly Cys Arg

1666 1676 1686 1696 1706 1716 1726
 ATATACACAC CACACACACA CACCACATAC ACCACACACA CACGTTCCCA TCCACTCACC CACACACTAC

1736 1746 1756 1766 1776 1786 1796
 ACAGACTGCT TCCTTATAGC TGGACTTTTA TTTAAAAAAA AAAAAAAAAA AATGGAAAAA ATCCCTAAAC

1806 1816 1826 1836 1846 1856 1866
 ATTCACCTTG ACCTTATTTA TGACTTTACG TGCAAATGTT TTGACCATAT TGATCATATA TTTTGACAAA

1876 1886 1896 1906 1916 1926 1936
 ATATATTTAT AACTACGTAT TAAAAGAAAA AAATAAAATG AGTCATTATT TTAACAAAAA AAAAAAACT

1946
 CTAGAGTCGA CGGAATTC

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FIGURE 3A

10 20 30 40 50
 GTGACCGAGC GCGCGGACG GCCGCCTGCC CCCTCTGCCA CCTGGGGCGG

60 70 80 90 99
 TGCGGGCCCC GAGCCCGGAG CCCGGGTAGC GCGTAGAGCC GCGCGC ATG
 MET
 (1)

108 117 126 135 144
 CAC GTG CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG
 His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala

153 162 171 180 189
 CTC TGG GCA CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC
 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe

198 207 216 225 234
 AGC CTG GAC AAC GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC
 Ser Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu

243 252 261 270 279
 CGC AGC CAG GAG CGG CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT
 Arg Ser Gln Glu Arg Arg Glu MET Gln Arg Glu Ile Leu Ser Ile

288 297 306 315 324
 TTG GGC TTG CCC CAC CGC CCG CGC CCG CAC CTC CAG GGC AAG CAC
 Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His

333 342 351 360 369
 AAC TCG GCA CCC ATG TTC ATG CTG GAC CTG TAC AAC GCC ATG GCG
 Asn Ser Ala Pro MET Phe MET Leu Asp Leu Tyr Asn Ala MET Ala

378 387 396 405 414
 GTG GAG GAG GGC GGC GGG CCC GGC GGC CAG GGC TTC TCC TAC CCC
 Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro

423 432 441 450 459
 TAC AAG GCC GTC TTC AGT ACC CAG GGC CCC CCT CTG GCC AGC CTC
 Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu

468 477 486 495 504
 CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC ATG GTC ATG AGC TTC
 Gln Asp Ser His Phe Leu Thr Asp Ala Asp MET Val MET Ser Phe

513 522 531 540 549
 GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC CAC CCA CGC TAC
 Val Asn Leu Val Glu His Asp Lys Glu Phe Phe His Pro Arg Tyr

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FIGURE 3B

558	567	576	585	594
CAC CAT CGA GAG TTC CGG TTT GAT CTT TCC AAG ATC CCA GAA GGG				
His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile Pro Glu Gly				
603	612	621	630	639
GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC TAC ATC				
Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Tyr Ile				
648	657	666	675	684
CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT CAG				
Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr Gln				
693	702	711	720	729
GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC				
Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu				
738	747	756	765	774
GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT				
Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe				
783	792	801	810	819
GAC ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC				
Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His				
828	837	846	855	864
AAC CTG GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC				
Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser				
873	882	891	900	909
ATC AAC CCC AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG				
Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln				
918	927	936	945	954
AAC AAG CAG CCC TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC				
Asn Lys Gln Pro Phe MET Val Ala Phe Phe Lys Ala Thr Glu Val				
963	972	981	990	999
CAC TTC CGC AGC ATC CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG				
His Phe Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln				
(293)				
1008	1017	1026	1035	1044
AAC CGC TCC AAG ACG CCC AAG AAC CAG GAA GCC CTG CGG ATG GCC				
Asn Arg Ser Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg MET Ala				
1053	1062	1071	1080	1089
AAC GTG GCA GAG AAC AGC AGC AGC GAC CAG AGG CAG GCC TGT AAG				
Asn Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys				

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FIGURE 3C

1098 1107 1116 1125 1134
 AAG CAC GAG CTG TAT GTC AGC TTC CGA GAC CTG GGC TGG CAG GAC
 Lys His Glu Leu Tyr Val Ser Phe Arg Asp Leu Gly Trp Gln Asp

1143 1152 1161 1170 1179
 TGG ATC ATC GCG CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGC
 Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly

1188 1197 1206 1215 1224
 GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC GCC ACC AAC CAC
 Glu Cys Ala Phe Pro Leu Asn Ser Tyr MET Asn Ala Thr Asn His

1233 1242 1251 1260 1269
 GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC CCG GAA ACG GTG
 Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro Ile Ser Val

1278 1287 1296 1305 1314
 CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC GTC
 Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser Val

1323 1332 1341 1350 1359
 CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA TAC AGA
 Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr Arg

1368 1377 1386 1399
 AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC
 Asn MET Val Val Arg Ala Cys Gly Cys His
 (431)

1409 1419 1429 1439 1448
 GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTC

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FIGURE 4A

10 20 30 40 50
 CGACCATGAG AGATAAGGAC TGAGGGCCAG GAAGGGGAAG CGAGCCCGCG

60 70 80 90 100
 GAGAGGTGGC GGGGACTGCT CACGCCAAGG GCCACAGCGG CCGCGCTCCG

110 120 130 140 150
 GCCTCGCTCC GCCGCTCCAC GCCTCGCGGG ATCCGCGGGG GCAGCCCGGG

159 168 177 186 195
 CGGGCGGGG ATG CCG GGG CTG GGG CGG AGG GCG CAG TGG CTG TGC
 MET Pro Gly Leu Gly Arg Arg Ala Gln Trp Leu Cys
 (1)

204 213 222 231 240
 TGG TGG TGG GGG CTG CTG TGC AGC TGC TGC GGG CCC CCG CCG CTG
 Trp Trp Trp Gly Leu Leu Cys Ser Cys Cys Gly Pro Pro Pro Leu

249 258 267 276 285
 CGG CCG CCC TTG CCC GCT GCC GCG GCC GCG GCC GCG GGG GGG CAG
 Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala Ala Ala Gly Gly Gln

294 303 312 321 330
 CTG CTG GGG GAC GGC GGG AGC CCC GGC CGC ACG GAG CAG CCG CCG
 Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr Glu Gln Pro Pro

339 348 357 366 375
 CCG TCG CCG CAG TCC TCC TCG GGC TTC CTG TAC CCG CCG CTC AAG
 Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg Arg Leu Lys

384 393 402 411 420
 ACG CAG GAG AAG CGG GAG ATG CAG AAG GAG ATC TTG TCG GTG CTG
 Thr Gln Glu Lys Arg Glu MET Gln Lys Glu Ile Leu Ser Val Leu

429 438 447 456 465
 GGG CTC CCG CAC CGG CCC CGG CCC CTG CAC GGC CTC CAA CAG CCG
 Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln Pro

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FIGURE 4B

474	483	492	501	510
CAG CCC CCG GCG CTC	CGG CAG CAG GAG GAG CAG	CAG CAG CAG CAG	CAG CAG CAG CAG	CAG CAG CAG CAG
Gln Pro Pro Ala Leu	Arg Gln Gln Glu Glu Gln	Gln Gln Gln Gln	Gln Gln Gln Gln	Gln Gln Gln Gln
519	528	537	546	555
CAG CTG CCT CGC GGA	GAG CCC CCT CCC GGG CGA	CTG AAG TCC GCG		
Gln Leu Pro Arg Gly	Glu Pro Pro Pro Gly Arg	Leu Lys Ser Ala		
564	573	582	591	600
CCC CTC TTC ATG CTG	GAT CTG TAC AAC GCC CTG	TCC GCC GAC AAC		
Pro Leu Phe MET Leu	Asp Leu Tyr Asn Ala Leu	Ser Ala Asp Asn		
609	618	627	636	645
GAC GAG GAC GGG GCG	TCG GAG GGG GAG AGG CAG	CAG TCC TGG CCC		
Asp Glu Asp Gly Ala	Ser Glu Gly Glu Arg Gln	Gln Ser Trp Pro		
654	663	672	681	690
CAC GAA GCA GCC AGC	TCG TCC CAG CGT CGG CAG	CCG CCC CCG GGC		
His Glu Ala Ala Ser	Ser Ser Gln Arg Arg Gln	Pro Pro Gly Ser		
699	708	717	726	735
GCC GCG CAC CCG CTC	AAC CGC AAG AGC CTT CTG	GCC CCC GGA TCT		
Pro Pro Gly Ala Ala	His Pro Leu Asn Arg Lys	Ser Leu Leu Ala		
744	753	762	771	780
GGC AGC GGC GGC GCG	TCC CCA CTG ACC AGC GCG	CAG GAC AGC GCC		
Gly Ser Gly Gly Ala	Ser Pro Leu Thr Ser Ala	Gln Asp Ser Ala		
789	798	807	816	825
TTC CTC AAC GAC GCG	GAC ATG GTC ATG AGC TTT	GTG AAC CTG GTG		
Phe Leu Asn Asp Ala	Asp MET Val MET Ser Phe	Val Asn Leu Val		
834	843	852	861	870
GAG TAC GAC AAG GAG	TTC TCC CCT CGT CAG CGA	CAC CAC AAA GAG		
Glu Tyr Asp Lys Glu	Phe Ser Pro Arg Gln Arg	His His Lys Glu		
879	888	897	906	915
TTC AAG TTC AAC TTA	TCC CAG ATT CCT GAG GGT	GAG GTG GTG ACG		
Phe Lys Phe Asn Leu	Ser Gln Ile Pro Glu Gly	Glu Val Val Thr		
924	933	942	951	960
GCT GCA GAA TTC CGC	ATC TAC AAG GAC TGT GTT	ATG GGG AGT TTT		
Phe Arg Ile Tyr Lys	Asp Cys Val MET Ala Ala	Glu Gly Ser Phe		

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FIGURE 4C

969 978 987 996 1005
 AAA AAC CAA ACT TTT CTT ATC AGC ATT TAT CAA GTC TTA CAG GAG
 Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr Gln Val Leu Gln Glu

1014 1023 1032 1041 1050
 CAT CAG CAC AGA GAC TCT GAC CTG TTT TTG TTG GAC ACC CGT GTA
 His Gln His Arg Asp Ser Asp Leu Phe Leu Leu Asp Thr Arg Val

1059 1068 1077 1086 1095
 GTA TGG GCC TCA GAA GAA GGC TGG CTG GAA TTT GAC ATC ACG GCC
 Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp Ile Thr Ala

1104 1113 1122 1131 1140
 ACT AGC AAT CTG TGG GTT GTG ACT CCA CAG CAT AAC ATG GGG CTT
 Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn MET Gly Leu

1149 1158 1167 1176 1185
 CAG CTG AGC GTG GTG ACA AGG GAT GGA GTC CAC GTC CAC CCC CGA
 Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro Arg

1194 1203 1212 1221 1230
 GCC GCA GGC CTG GTG GGC AGA GAC GGC CCT TAC GAT AAG CAG CCC
 Ala Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro

1239 1248 1257 1266 1275
 TTC ATG GTG GCT TTC TTC AAA GTG AGT GAG GTC CAC GTG CGC ACC
 Phe MET Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr

1284 1293 1302 1311 1320
 ACC AGG TCA GCC TCC AGC CGG CGC CGA CAA CAG AGT CGT AAT CGC
 Thr Arg Ser Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn Arg
 (382)

1329 1338 1347 1356 1365
 TCT ACC CAG TCC CAG GAC GTG GCG CGG GTC TCC AGT GCT TCA GAT
Ser Thr Gln Ser Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp
 (388)

1374 1383 1392 1401 1410
 TAC AAC AGC AGT GAA TTG AAA ACA GCC TGC AGG AAG CAT GAG CTG
 Tyr Asn Ser Ser Glu Leu Lys Thr Ala Cys Arg Lys His Glu Leu
 (412)

1419 1428 1437 1446 1455
 TAT GTG AGT TTC CAA GAC CTG GGA TGG CAG GAC TGG ATC ATT GCA
Tyr Val Ser Phe Gln Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala

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FIGURE 4D

1464	1473	1482	1491	1500
CCC AAG GGC TAT GCT GCC AAT TAC TGT GAT GGA GAA TGC TCC TTC				
Pro Lys Gly Tyr Ala Ala Asn Tyr Cys Asp Gly Glu Cys Ser Phe				
1509	1518	1527	1536	1545
CCA CTC AAC GCA CAC ATG AAT GCA ACC AAC CAC GCG ATT GTG CAG				
Pro Leu Asn Ala His MET Asn Ala Thr Asn His Ala Ile Val Gln				
1554	1563	1572	1581	1590
ACC TTG GTT CAC CTT ATG AAC CCC GAG TAT GTC CCC AAA CCG TGC				
Thr Leu Val His Leu MET Asn Pro Glu Tyr Val Pro Lys Pro Cys				
1599	1608	1617	1626	1635
TGT GCG CCA ACT AAG CTA AAT GCC ATC TCG GTT CTT TAC TTT GAT				
Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp				
1644	1653	1662	1671	1680
GAC AAC TCC AAT GTC ATT CTG AAA AAA TAC AGG AAT ATG GTT GTA				
Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg Asn MET Val Val				
1689	1698	1708	1718	1728
AGA GCT TGT GGA TGC CAC TAACTCGAAA CCAGATGCTG GGGACACACA				
Arg Ala Cys Gly Cys His				
(513)				
1738	1748	1758	1768	1778
TTCTGCCTTG GATTCCTAGA TTACATCTGC CTTAAAAAAA CACGGAAGCA				
1788	1798	1808	1818	1828
CAGTTGGAGG TGGGACGATG AGACTTTGAA ACTATCTCAT GCCAGTGCCT				
1838	1848	1858	1868	1878
TATTACCCAG GAAGATTTTA AAGGACCTCA TTAATAATTT GCTCACTTGG				
1888	1898	1908	1918	1928
TAAATGACGT GAGTAGTTGT TGGTCTGTAG CAAGCTGAGT TTGGATGTCT				
1938	1948	1958	1968	1978
GTAGCATAAG GTCTGGTAAC TGCAGAAACA TAACCGTGAA GCTCTTCCTA				
1988	1998	2008	2018	2028
CCCTCCTCCC CCAAAAACCC ACCAAAATTA GTTTTAGCTG TAGATCAAGC				
2038	2048	2058	2068	2078
TATTTGGGGT GTTTGTAGT AAATAGGGAA AATAATCTCA AAGGAGTTAA				
2088	2098	2108	2118	2128
ATGTATTCTT GGCTAAAGGA TCAGCTGGTT CAGTACTGTC TATCAAAGGT				

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FIGURE 4E

2138	2148	2158	2168	2178
AGATTTTACA	GAGAACAGAA	ATCGGGGAAG	TGGGGGGAAC	GCCTCTGTTC
2188	2198	2208	2218	2228
AGTTCATTCC	CAGAAGTCCA	CAGGACGCAC	AGCCCAGGCC	ACAGCCAGGG
2238	2248	2258	2268	2278
CTCCACGGGG	CGCCCTTGTC	TCAGTCATTG	CTGTTGTATG	TTCGTGCTGG
2288	2298	2308	2318	2328
AGTTTTGTTG	GTGTGAAAAT	ACACTTATTT	CAGCCAAAAC	ATACCATTTC
2338	2348	2358	2368	2378
TACACCTCAA	TCCTCCATTT	GCTGTACTCT	TTGCTAGTAC	CAAAAGTAGA
2388	2398	2408	2418	2428
CTGATTACAC	TGAGGTGAGG	CTACAAGGGG	TGTGTAACCG	TGTAACACGT
2438	2448	2458	2468	2478
GAAGGCAGTG	CTCACCTCTT	CTTTACCAGA	ACGGTTCTTT	GACCAGCACA
2488	2498	2508	2518	2528
TTAACTTCTG	GACTGCCGGC	TCTAGTACCT	TTTCAGTAAA	GTGGTTCTCT
2538	2548	2558	2568	2578
GCCTTTTTTAC	TATACAGCAT	ACCACGCCAC	AGGGTTAGAA	CCAACGAAGA
2588	2598	2608	2618	2628
AAATAAAATG	AGGGTGCCCA	GCTTATAAGA	ATGGTGTTAG	GGGGATGAGC
2638	2648	2658	2668	2678
ATGCTGTTTA	TGAACGGAAA	TCATGATTTT	CCTGTAGAAA	GTGAGGCTCA
2688	2698	2708	2718	2728
GATTAAATTT	TAGAATATTT	TCTAAATGTC	TTTTTCACAA	TCATGTGACT
2738	2748	2758	2768	2778
GGGAAGGCAA	TTTCATACTA	AACTGATTAA	ATAATACATT	TATAATCTAC
2788	2798	2808	2818	2828
AACTGTTTGC	ACTTACAGCT	TTTTTTGTAA	ATATAAACTA	TAATTTATTG
2838	2848	2858	2868	2878
TCTATTTTAT	ATCTGTTTTG	CTGTGGCGTT	GGGGGGGGGG	CCGGGCTTTT
2888	2898	2908	2918	
GGGGGGGGGG	GTTTGTGTTGG	GGGGTGTCTG	GGTGTGGGCG	GGCGG

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FIGURE 5A

10	20	30	40	50
CTGGTATATT	TGTGCCTGCT	GGAGGTGGAA	TTAACAGTAA	GAAGGAGAAA
60	70	80	90	100
GGGATTGAAT	GGACTTACAG	GAAGGATTTTC	AAGTAAATTC	AGGGAAACAC
110	120	130	140	150
ATTTACTTGA	ATAGTACAAC	CTAGAGTATT	ATTTTACACT	AAGACGACAC
160	170	180	190	200
AAAAGATGTT	AAAGTTATCA	CCAAGCTGCC	GGACAGATAT	ATATTCCAAC
210	220	230	240	250
ACCAAGGTGC	AGATCAGCAT	AGATCTGTGA	TTCAGAAATC	AGGATTTGTT
260	270	280	290	300
TTGGAAAGAG	CTCAAGGGTT	GAGAAGAACT	CAAAAGCAAG	TGAAGATTAC
310	320	330	340	350
TTTGGGAAC	ACAGTTTATC	AGAAGATCAA	CTTTTGCTAA	TTCAAATACC
360	370	380	390	400
AAAGGCCTGA	TTATCATAAA	TTCATATAGG	AATGCATAGG	TCATCTGATC
410	420	430	440	450
AAATAATATT	AGCCGTCTTC	TGCTACATCA	ATGCAGCAAA	AACTCTTAAC
460	470	480	490	500
AACTGTGGAT	AATTGGAAAT	CTGAGTTTCA	GCTTTCTTAG	AAATAACTAC
510	520	530	540	550
TCTTGACATA	TTCCAAAATA	TTTAAATAG	GACAGGAAAA	TCGGTGAGGA
560	570	580	590	600
TGTTGTGCTC	AGAAATGTCA	CTGTCATGAA	AAATAGGTAA	ATTTGTTTTT
610	620	630	640	650
TCAGCTACTG	GGAAACTGTA	CCTCCTAGAA	CCTTAGGTTT	TTTTTTTTTT
660	670	680	690	700
AAGAGGACAA	GAAGGACTAA	AAATATCAAC	TTTTGCTTTT	GGACAAAA

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FIGURE 5B

701	710	719	728	737
ATG CAT CTG ACT GTA TTT TTA CTT AAG GGT ATT GTG GGT TTC CTC				
MET His Leu Thr Val Phe Leu Leu Lys Gly Ile Val Gly Phe Leu				
(1)				
746	755	764	773	782
TGG AGC TGC TGG GTT CTA GTG GGT TAT GCA AAA GGA GGT TTG GGA				
Trp Ser Cys Trp Val Leu Val Gly Tyr Ala Lys Gly Gly Leu Gly				
791	800	809	818	827
GAC AAT CAT GTT CAC TCC AGT TTT ATT TAT AGA AGA CTA CGG AAC				
Asp Asn His Val His Ser Ser Phe Ile Tyr Arg Arg Leu Arg Asn				
836	845	854	863	872
CAC GAA AGA CGG GAA ATA CAA AGG GAA ATT CTC TCT ATC TTG GGT				
His Glu Arg Arg Glu Ile Gln Arg Glu Ile Leu Ser Ile Leu Gly				
881	890	899	908	917
TTG CCT CAC AGA CCC AGA CCA TTT TCA CCT GGA AAA ATG ACC AAT				
Leu Pro His Arg Pro Arg Pro Phe Ser Pro Gly Lys Gln Ala Ser				
926	935	944	953	962
CAA GCG TCC TCT GCA CCT CTC TTT ATG CTG GAT CTC TAC AAT GCC				
Ser Ala Pro Leu Phe MET Leu Asp Leu Tyr Asn Ala MET Thr Asn				
971	980	989	998	1007
GAA GAA AAT CCT GAA GAG TCG GAG TAC TCA GTA AGG GCA TCC TTG				
Glu Glu Asn Pro Glu Glu Ser Glu Tyr Ser Val Arg Ala Ser Leu				
1016	1025	1034	1043	1052
GCA GAA GAG ACC AGA GGG GCA AGA AAG GGA TAC CCA GCC TCT CCC				
Ala Glu Glu Thr Arg Gly Ala Arg Lys Gly Tyr Pro Ala Ser Pro				
1061	1070	1079	1088	1097
AAT GGG TAT CCT CGT CGC ATA CAG TTA TCT CGG ACG ACT CCT CTG				
Asn Gly Tyr Pro Arg Arg Ile Gln Leu Ser Arg Thr Thr Pro Leu				
1106	1115	1124	1133	1142
ACC ACC CAG AGT CCT CCT CTA GCC AGC CTC CAT GAT ACC AAC TTT				
Thr Thr Gln Ser Pro Pro Leu Ala Ser Leu His Asp Thr Asn Phe				
1151	1160	1169	1178	1187
CTG AAT GAT GCT GAC ATG GTC ATG AGC TTT GTC AAC TTA GTT GAA				
Leu Asn Asp Ala Asp MET Val MET Ser Phe Val Asn Leu Val Glu				
1196	1205	1214	1223	1232
AGA GAC AAG GAT TTT TCT CAC CAG CGA AGG CAT TAC AAA GAA TTT				
Arg Asp Lys Asp Phe Ser His Gln Arg Arg His Tyr Lys Glu Phe				

FIGURE 5C

1241	1250	1259	1268	1277
CGA TTT GAT CTT ACC CAA ATT CCT CAT GGA GAG GCA GTG ACA GCA				
Arg Phe Asp Leu Thr Gln Ile Pro His Gly Glu Ala Val Thr Ala				
1286	1295	1304	1313	1322
GCT GAA TTC CGG ATA TAC AAG GAC CGG AGC AAC AAC CGA TTT GAA				
Ala Glu Phe Arg Ile Tyr Lys Asp Arg Ser Asn Asn Arg Phe Glu				
1331	1340	1349	1358	1367
AAT GAA ACA ATT AAG ATT AGC ATA TAT CAA ATC ATC AAG GAA TAC				
Asn Glu Thr Ile Lys Ile Ser Ile Tyr Gln Ile Ile Lys Glu Tyr				
1376	1385	1394	1403	1412
ACA AAT AGG GAT GCA GAT CTG TTC TTG TTA GAC ACA AGA AAG GCC				
Thr Asn Arg Asp Ala Asp Leu Phe Leu Leu Asp Thr Arg Lys Ala				
1421	1430	1439	1448	1457
CAA GCT TTA GAT GTG GGT TGG CTT GTC TTT GAT ATC ACT GTG ACC				
Gln Ala Leu Asp Val Gly Trp Leu Val Phe Asp Ile Thr Val Thr				
1466	1475	1484	1493	1502
AGC AAT CAT TGG GTG ATT AAT CCC CAG AAT AAT TTG GGC TTA CAG				
Ser Asn His Trp Val Ile Asn Pro Gln Asn Asn Leu Gly Leu Gln				
1511	1520	1529	1538	1547
CTC TGT GCA GAA ACA GGG GAT GGA CGC AGT ATC AAC GTA AAA TCT				
Leu Cys Ala Glu Thr Gly Asp Gly Arg Ser Ile Asn Val Lys Ser				
1556	1565	1574	1583	1592
GCT GGT CTT GTG GGA AGA CAG GGA CCT CAG TCA AAA CAA CCA TTC				
Ala Gly Leu Val Gly Arg Gln Gly Pro Gln Ser Lys Gln Pro Phe				
1601	1610	1619	1628	1637
ATG GTG GCC TTC TTC AAG GCG AGT GAG GTA CTT CTT CGA TCC GTG				
MET Val Ala Phe Phe Lys Ala Ser Glu Val Leu Leu Arg Ser Val				
1646	1655	1664	1673	1682
AGA GCA GCC AAC AAA CGA AAA AAT CAA AAC CGC AAT AAA TCC AGC				
Arg Ala Ala Asn Lys Arg Lys Asn Gln Asn Arg Asn Lys <u>Ser Ser</u>				
				(329)
1691	1700	1709	1718	1727
TCT CAT CAG GAC TCC TCC AGA ATG TCC AGT GTT GGA GAT TAT AAC				
<u>Ser His Gln Asp Ser Ser Arg MET Ser Ser Val Gly Asp Tyr Asn</u>				
				(337)

FIGURE 5D

2110 2120 2130 2140 2150
TAAGGTTTAT GGCTGCAATA AAAAGCATAC TTTTCAGACAA ACAGAAAAAA AAA

Figure 6

(1)
GAATTCC GAG CCC CAT TGG AAG GAG TTC CGC TTT GAC CTG ACC CAG ATC CCG GCT
Glu Pro His Trp Lys Glu Phe Arg Phe Asp Leu Thr Gln Ile Pro Ala
(10)

GGG GAG GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG GTG CCC AGC ATC CAC
Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Val Pro Ser Ile His
(20)

CTG CTC AAC AGG ACC CTC CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG TCC
Leu Leu Asn Arg Thr Leu His Val Ser Met Phe Gln Val Val Gln Glu Gln Ser
(40)

AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG ACG CTC CGA GCT GGA GAC
Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln Thr Leu Arg Ala Gly Asp
(60)

GAG GGC TGG CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC TGG TTG CTG AAG
Glu Gly Typ Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys Trp Leu Leu Lys
(80)

CGT CAC AAG GAC CTG GGA CTC CGC CTC TAT GTG GAG ACT GAG GAT GGG CAC AGC
Arg His Lys Asp Leu Gly Lue Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser
(90)

GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT CAA CGG GCC CCA CGC TCC CAA CAG
Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln Arg Ala Pro Arg Ser Gln Gln
(110)

CCT TTC GTG GTC ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC ACC CCT CGG
Pro Phe Val Val Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg Thr Pro Arg
(130)

GCA GTG AGG CCA CTG AGG AGG AGG CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG
Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln
(150)

GCC AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC GGC TCC CAC GGC CGG CAG
Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser His Gly Arg Gln
(170)

GTC TGC CGT CGG CAC GAG CTC TAC GTC AGC TTC CAG GAC CTT GGC TGG CTG GAC
Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp
(180)

TGG GTC ATC GCC CCC CAA GGC TAC TCA GCC TAT TAC TGT GAG GGG GAG TGC TCC
Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys Ser
(200)

TTC CCG CTG GAC TCC TGC ATG AAC GCC ACC AAC CAC GCC ATC CTG CAG TCC CTG
Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu Gln Ser Leu
(220)

(230)

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Figure 6 (Con't)

GTG CAC CTG ATG AAG CCA AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC AAG
Val His Leu Met Lys Pro Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys
(240) (250)

CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC AGC AGC AAC AAC GTC ATC CTG CGC
Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg
(260)

AAG CAC CGC AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC TGAGTCAGCCCCGCCAGC
Lys His Arg Asn Met Val Val Lys Ala Cys Gly Cys His
(270) (280)

CCTACTGCAGCCACCCTTCTCATCTGGATCGGGCCCTGCAGAGGCAGAAAACCCTTAAATGCTGTCACAG
CTCAAGCAGGAGTGTCAGGGGCCCTCACTCTCGGTGCCTACTTCCTGTCAGGCTTCTGGGAATTC

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FIGURE 7

GACGAAAGGG CCTCCTGATA GCGCTATTTT TATAGGTTAA TGTCATGATA ATAATGGTTT 60
 CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG AACCCGTATT TGTTTATTTT 120
 TCTAAATACA TTCAAATATG TATCCGCTCA TGAGACAATA ACOOTGATAA ATGCTTCAAT 180
 AATATTGAAA AAGGAAAGAGT ATGAGTATTC AACATTTGCG TGTCGCGCTT ATTCCCTTTT 240
 TTGCGGCAAT TTGCTTTCCT GTTTTTGCTC ACCCAGAAAC GCTGCTGAAA GTAAAGATG 300
 CTGAAGATCA GTTGGGTGCA CGAGTGGGT ACATCGAACT GATCTCAAC AGCGGTAAAG 360
 TCCTTGAGAG TTTTCCCCC GAAGAACGTT TTCCAATGAT GAGCACTTTT AAGTTCTGC 420
 TATGTGCGGC GGTATTATCC GGTATTGACC CCGGCAAGA GCAACTCGGT CGCCGCATAC 480
 ACTATTGTCA GAATGACTTG GTTGAGTACT CACCACTGAC AGAAAAGCAT CTTACGGATG 520
 GGATGACAGT AAGAGAATTA TGCAGTCTG CGATAACCAT GAGTGATAAC ACTGCGGCCA 600
 ACTTACTTCT GACAACGATC GAGGACCGA ACGAGCTAAC CGCTTTTTTG CACAACATGG 660
 GCGATCATGT AACTCGCCTT GATCGTTGGG AACCGAGGT GAATGAAGCC ATACCAAGC 720
 ACGAGCGTGA CACCACGATG CGTGTAGCAA TGGCAACAAC GTTGGCGAAA CTATTAACTG 780
 GCGAACTACT TACTCTAGCT TCCCGGCAAC AATTAATAGA GTGGATGGAG GCGGATAAAG 840
 TTGCAAGACC ACTTCTGCGC TCGGCCCTTC CCGCTGGCTG GTTTATTGCT GATAAATCTG 900
 GAGCGCGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GCGGCGAGAT GGTAAAGCCT 960
 CCGGTATCGT AGTTATCTAC ACGACGGGGA GTCAAGCAAC TATGGATGAA CGAATAGAC 1020
 AGATCGCTGA GATAGGTGCC TCACTGATTA AGCATTGGTA ACTGTCAGAC CAAGTTTACT 1080
 CATATATACT TTAGATTGAT TTAAACTTC ATTTTAAAT TAAAGGATC TAGGTGAGA 1140
 TCCTTTTTGA TAATCTCATG ACCAAATCC CTTAACGTGA GTTTTCGTC CACTGAGCGT 1200
 CAGACCCCGT AGAAAAGATC AAGGATCTT CTTGAGATCC TTTTTTCTG GCGTAACTT 1260
 GCTGCTTGCA AACAAAAAA CCACCGTAC CAGCGGTGGT TTGTTTGCCG GATCAAGAGC 1320
 TAACAACTCT TTTTCCGAG GTAAGTGGCT TCAGCAGAGC GCAGATACCA AATACTGTCC 1380
 TTCTAGTGTG GCCGTAGTTA GCGCACACT TCAAGAACTC TGTAGCAGCG COTACATACC 1440
 TCGTCTGCT AATGCTGTTA CCACTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG 1500
 GGTGGACTC AAGACGATAG TTACCAGATA AGGCGCAGCG GTGCGGCTGA ACGGGCGGTT 1560
 CGTGACACA GCGCAGCTTG GAGCGAACGA COTAGACGA ACTGAGATAC CTACAGCGTG 1620
 AGCATTGAGA AAGCGCCACC CTTCCGAGG GAGAGAAAGC GGACAGGTAT CCGGTAGAGC 1680
 GCAGGCTCGG AACAGGAGAG CGCACGAGG ACCTTCCAGG GGGAAACGCC TGGTATCTTT 1740
 ATAGTCTGT CCGGTTTTCG CACCTCTGAC TTGAGCGTCG ATTTTGTGA TGCTGCTCAG 1800
 GCGGGCGGAG CCTATCGAAA AACGCCAGCA ACGCGGCTT TTTACGGTC CTGCGCTTTT 1860
 GCTGCGCTT TGCTCACATG TTCTTTCCTG CGTTATCCCG TGATTCTGTG GATAACCGTA 1920

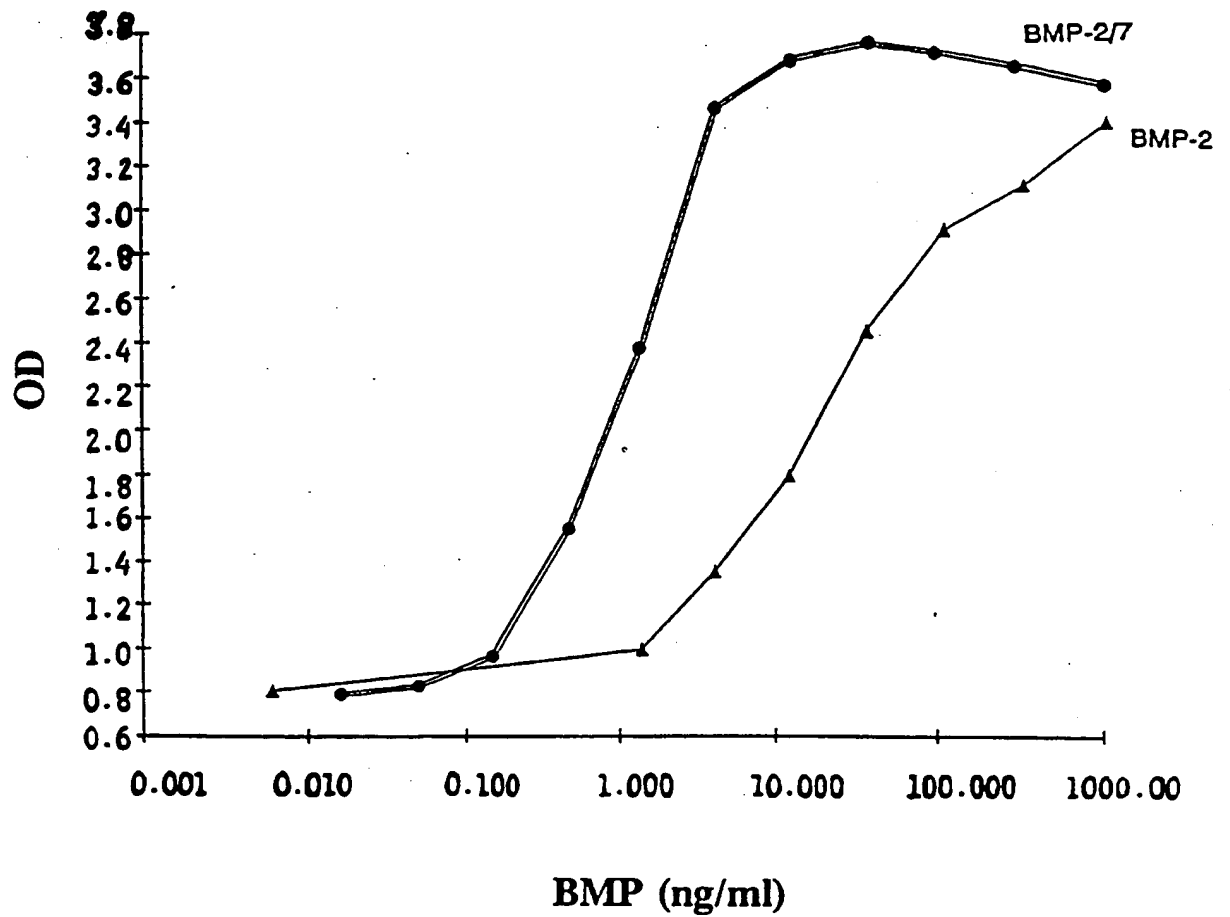
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FIGURE 7 (cont'd)

TTACCGCCTT TGAAGTACCT GATACCGCTC GCGCGAGCCG AACGACCGAG CCGACCGAGT 1980
 CAGTGAGCGA CGAAGCGGAA GAGCGCCGAA TACGCAACC GCCTCTCCCG CCGCGTTGGC 2040
 CGATTCATTA ATGCAGAATT GATCTCTCAC CTACCAACA ATGCCCCCTT CCAAAAAATA 2100
 AATTCATATA AAAAACATAC AGATAACCAT CTGCGGTGAT AAATTATCTC TGGCGGTGTT 2160
 GACATAAATA CCACTGGCGG TGATACTGAG CACATCAGCA GGACGCACTG ACCACCATGA 2220
 AGGTGACGCT CTTAAAAATT AAGCCCTGAA GAAGGCGAGC ATTCAAAGCA GAAGGCTTTG 2280
 GGGTGTCTGA TACGAAACGA AGCATTGGCC GTAAGTGCGA TTCGGGATTA GCTGCGAATG 2340
 TGCCAAATCGC GGGGCGTTTT CGTTCAGGAC TACAACTGCC ACACACCACC AAAGCTAACT 2400
 GACAGGAGAA TCCAGATGCA TGCACAACA CCGCGCCGCG AACGTCCGCG AGAGAAACAG 2460
 GCTCAATGGA AAGCAGCAAA TCCCCTGTTG GTTGGGTTAA GCGCAAAACC AGTTCGAAA 2520
 GATTTTTTTA ACTATAACG CTGATCGAAG CGTTTATGCG GAAGAGCTAA AGCCCTTCCC 2580
 GAGTAACAAA AAAACAACAG CXTAAATAAC CCGCTCTTA CACATTCCAG CCCTGAAAAA 2640
 GGGCATCAAA TTAACCACA CCTATGGTGT ATGCATTTAT TGCATACAT TCAATGAATT 2700
 GTTATCTAAG GAAATACTTA CATATGCAAG CTAACATAA ACAACGTAA CGTCTGAAAT 2760
 CTAGCTGTAA GAGACACCGT TTGTAGCTGG ACTTCAGTGA CGTGGGTTGG AATGACTGGA 2820
 TTGTGGCTCC CCGCGGTAT CACGCTTTT ACTGCCAGG AGAATGCCCT TTTCCTCTGG 2880
 CTGATCATCT GAATCCACT AATCATGCA TTGTTCAAGC GTTGGTCAAC TCTGTTAACT 2940
 CTAAGATTCC TAAGGCATG TGTGTCCGA CAGAACTCA TGTATCTCG ATGCTGTACC 3000
 TTGAGAGAA TGAAGGTT GTATTAAAG ACTATCAGA CATGTTTGTG GAGGCTTGTG 3060
 GGTGTGCTA GTACAGCAAA ATTAATACA TAAATATATA TATATATATA TATTTTAA 3120
 AAAAGAAAA AATCTAGAGT CGACCTGAG TAATCOTACA GGTAGTACA AATAAAAAAG 3180
 GCAAGTCAGA TGACGTGCTT TTTTCTTGT GAGCAGTAAG CTTGCACTG CCGCTCCTTT 3240
 TACAAGCTCG TGACTGGGA AACCTGCGG TTAGCCAACT TAATCGCCTT GCAAGCATC 3300
 CCCCTTTGCG CAGCTGGCGT AATAGCGAAG AGGCGGCGAC CGATCGCCCT TCCCAACAGT 3360
 TGCGCAGCCT GAATGCGGAA TGGCGGCTGA TGCGGTATTT TCTCCTTACG CATCTGTGCG 3420
 GTATTTTACA CCGCATATAT GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT 3480
 AAGCCAGCCC CGACAGCCCG CAACAGCCCG TGACGCGCCC TGAGGGCTT GTCTGCTCCC 3540
 GGCATCCGCT TACAGACAAG CTGTGACCGT CTGCGGAGC TGCAATGTGC AGAGGTTTTT 3600
 ACCGTCACTA CCGAAACCGG CGA 3623

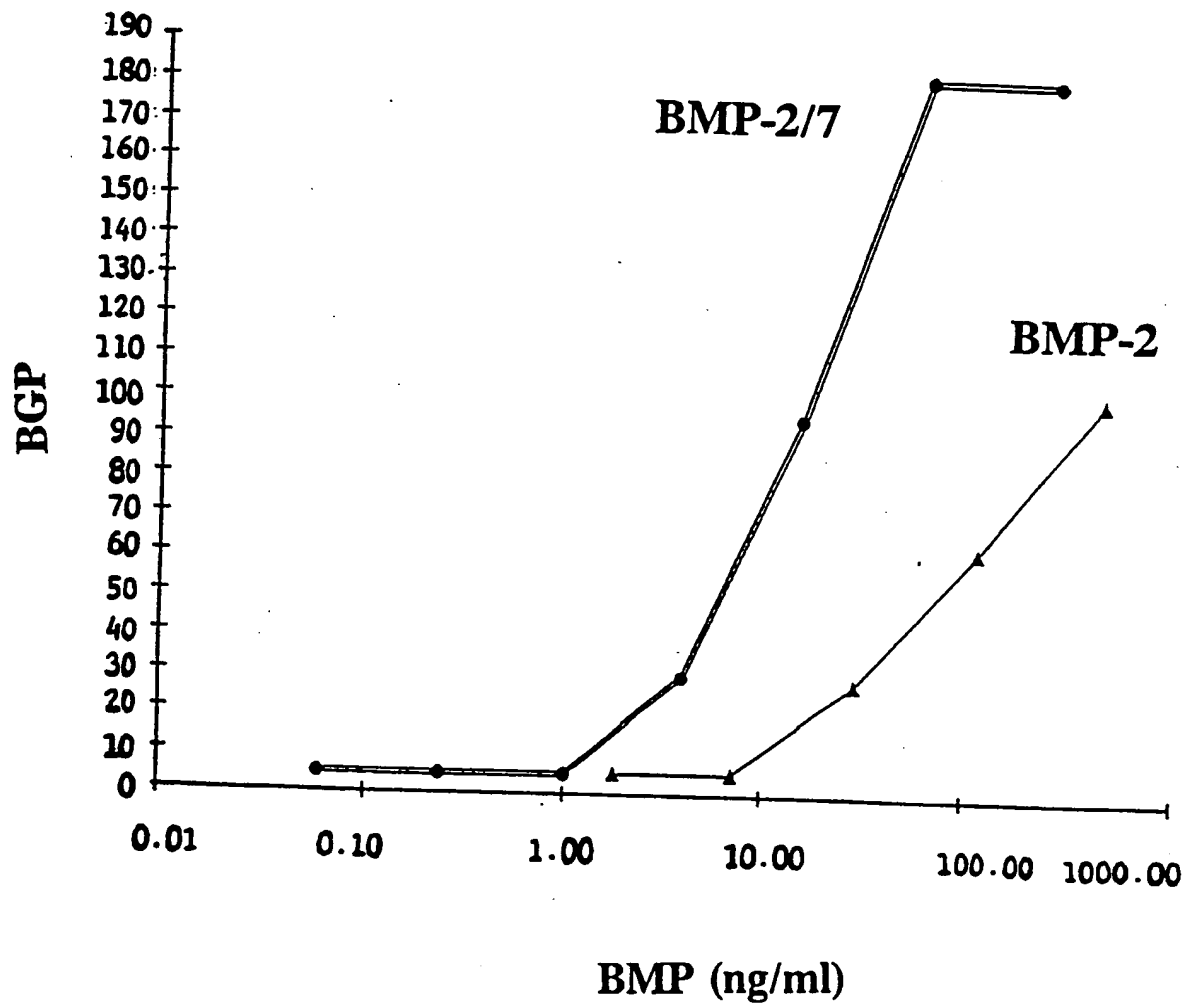
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FIGURE 8**W-20 ALKALINE PHOSPHATASE: BMP-2 VS. BMP-2/7**

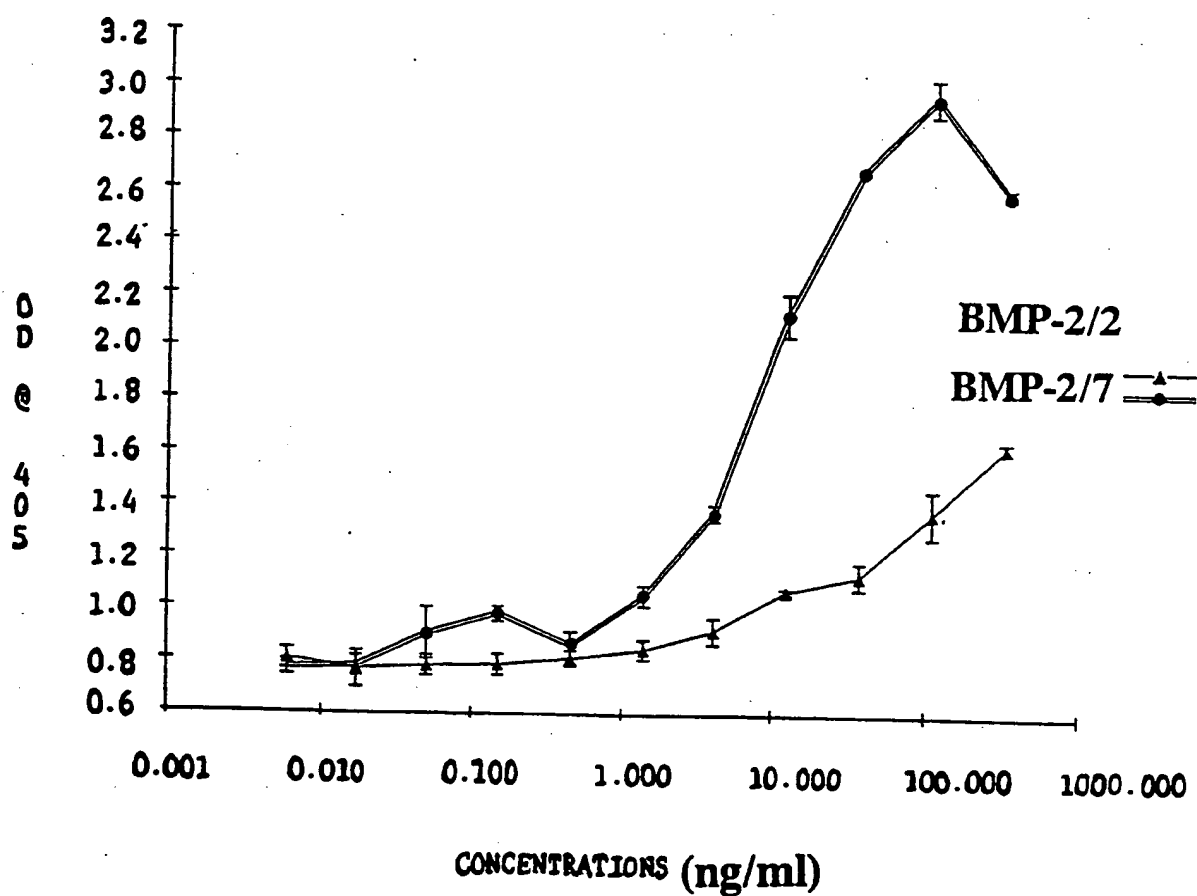
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FIGURE 9**EFFECTS OF BMP-2 AND BMP2/7 ON BGP SYNTHESIS BY W-20 CELLS**

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FIGURE 10**COMPARAISON OF *E. Coli* BMP-2 AND BMP-2/7:
W-20-17 ALKALINE PHOSPHATASE**

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FIGURE 11A

10 20 30 40 50 60 70
 AGATCTTGAA AACACCCGGG CCACACAAGC OGOGAOCCTAC AGCTCTTTCT CAGOGTTGGA GTGGAGAOGG
 80 90 100 110 120 130 140
 OGCCCGCAGC GCGCTGCGCG GGTGAGGTCC GCGCAGCTGC TGGGGAAGAG CCCAOCCTGC AGGCTGCGCT
 150 160 170 180 190 200 210
 GGGTCAGCGC AGCAAGTGGG GCTGGCGGCT ATCTGCGTGC AOCGGGCGC GTCCCGGGCT CCGTGGCGCC
 220 230 240 250 260 270 280
 TCGCCCGCAGC TGGTTTGGAG TTCAAOCCTC GGCTCCGCGC CCGGCTCCTT GCGCTTCGG AGTGTCGGC
 290 300 310 320 (1) 335
 AGOGAOCGCG GGAGCCGAAG CGCGCGCGG GTACCTAGCC ATG GCT GGG GCG AGC AGG CTG CTC
 MET Ala Gly Ala Ser Arg Leu Leu
 350 365 380 395
 TTT CTG TGG CTG GGC TGC TTC TGC GTG AGC CTG GCG CAG GGA GAG AGA CCG AAG CCA
 Phe Leu Trp Leu Gly Cys Phe Cys Val Ser Leu Ala Gln Gly Glu Arg Pro Lys Pro
 410 425 440 455
 CCT TTC CCG GAG CTC GCG AAA GCT GTG CCA GGT GAC GCG ACG GCA GGT GGT GGC CCG
 Pro Phe Pro Glu Leu Arg Lys Ala Val Pro Gly Asp Arg Thr Ala Gly Gly Gly Pro
 470 485 500 515
 GAC TCC GAG CTG CAG CCG CAA GAC AAG GTC TCT GAA CAC ATG CTG CCG CTC TAT GAC
 Asp Ser Glu Leu Gln Pro Gln Asp Lys Val Ser Glu His MET Leu Arg Leu Tyr Asp
 530 545 560
 AGG TAC AGC ACG GTC CAG GCG GCC CCG ACA CCG GGC TCC CTG GAG GGA GGC TCG CAG
 Arg Tyr Ser Thr Val Gln Ala Ala Arg Thr Pro Gly Ser Leu Glu Gly Gly Ser Gln
 575 590 605 620
 CCC TGG CCG CCT CCG CTC CTG CCG GAA GGC AAC ACG GTT CCG AGC TTT CCG GCG GCA
 Pro Trp Arg Pro Arg Leu Leu Arg Glu Gly Asn Thr Val Arg Ser Phe Arg Ala Ala
 635 650 665 680
 GCA GCA GAA ACT CTT GAA AGA AAA GGA CTG TAT ATC TTC AAT CTG ACA TCG CTA ACC
 Ala Ala Glu Thr Leu Glu Arg Lys Gly Leu Tyr Ile Phe Asn Leu Thr Ser Leu Thr
 695 710 725 740
 AAG TCT GAA AAC ATT TTG TCT GCG ACA CTG TAT TTC TGT ATT GGA GAG CTA GGA AAC
 Lys Ser Glu Asn Ile Leu Ser Ala Thr Leu Tyr Phe Cys Ile Gly Glu Leu Gly Asn

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FIGURE 11C

1430 1445 (377) 1460 1475
 TGC GOC AGG AGA TAC CTC AAG GTA GAC TTT GCA GAT ATT GGC TGG AGT GAA TGG ATT
 Cys Ala Arg Arg Tyr Leu Lys Val Asp Phe Ala Asp Ile Gly Trp Ser Glu Trp Ile

 1490 1505 1520 1535
 ATC TOC CQC AAG TOC TTT GAT GOC TAT TAT TGC TCT GGA GCA TGC CAG TTC CQC ATG
 Ile Ser Pro Lys Ser Phe Asp Ala Tyr Tyr Cys Ser Gly Ala Cys Gln Phe Pro MET

 1550 1565 1580 1595
 CCA AAG TCT TTG AAG CCA TCA AAT CAT GCT ACC ATC CAG AGT ATA GTG AGA GCT GTG
 Pro Lys Ser Leu Lys Pro Ser Asn His Ala Thr Ile Gln Ser Ile Val Arg Ala Val

 1610 1625 1640 1655
 GGG GTC GTT OCT GGG ATT OCT GAG OCT TGC TGT GTA CCA GAA AAG ATG TOC TCA CTC
 Gly Val Val Pro Gly Ile Pro Glu Pro Cys Cys Val Pro Glu Lys MET Ser Ser Leu

 1670 1685 1700
 AGT ATT TTA TTC TTT GAT GAA AAT AAG AAT GTA GTG CTT AAA GTA TAC OCT AAC ATG
 Ser Ile Leu Phe Phe Asp Glu Asn Lys Asn Val Val Leu Lys Val Tyr Pro Asn MET

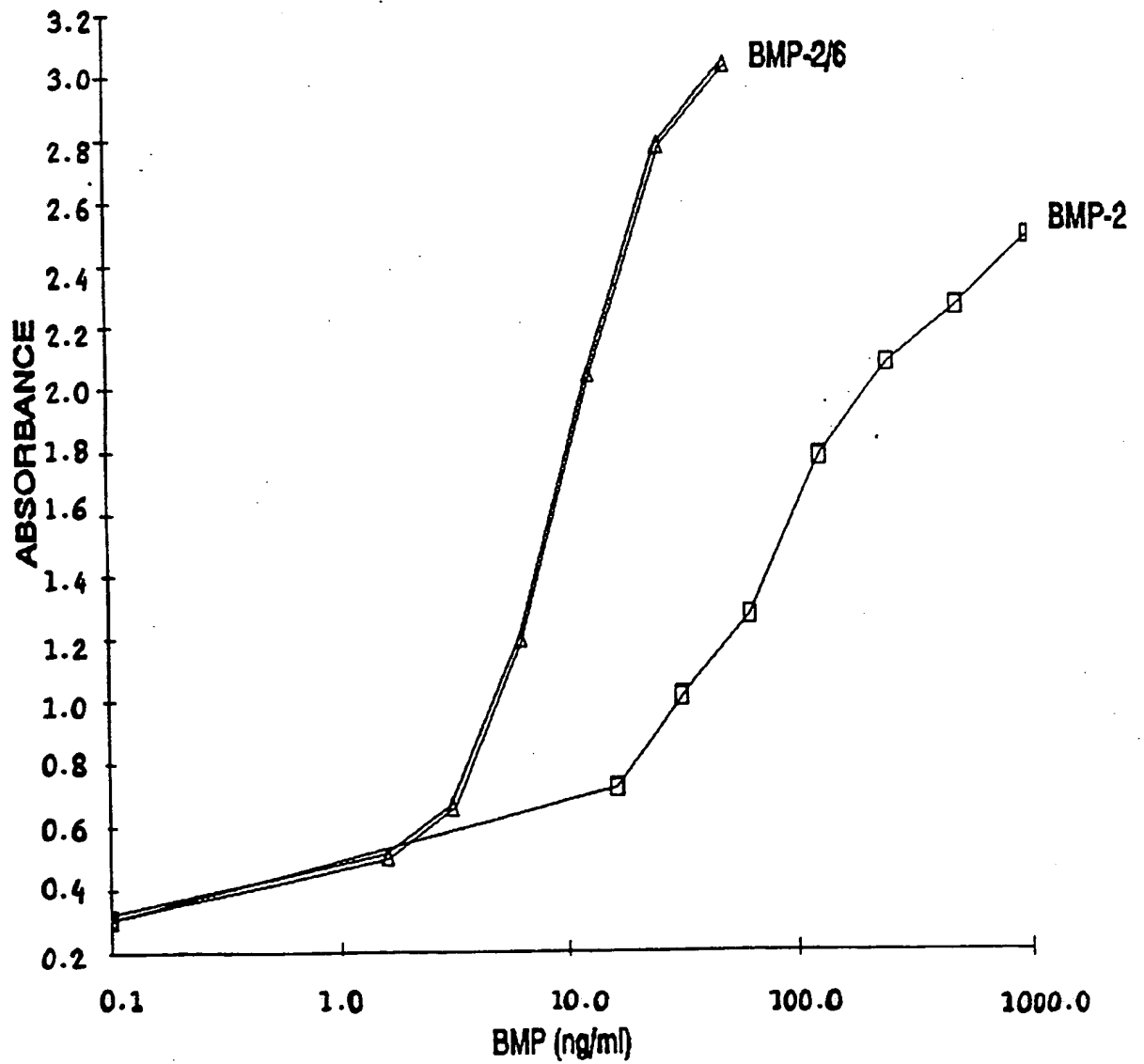
1715 1730 (472) 1746 1756 1766 1776
 ACA GTA GAG TCT TGC GCT TGC AGA TAACCTGGCA AAGAACTCAT TTGAATGCTT AATTCAATCT
Thr Val Glu Ser Cys Ala Cys Arg

 1786
 CTAGAGTGA CGGAATTC

SUBSTITUTE SHEET

Figure 12

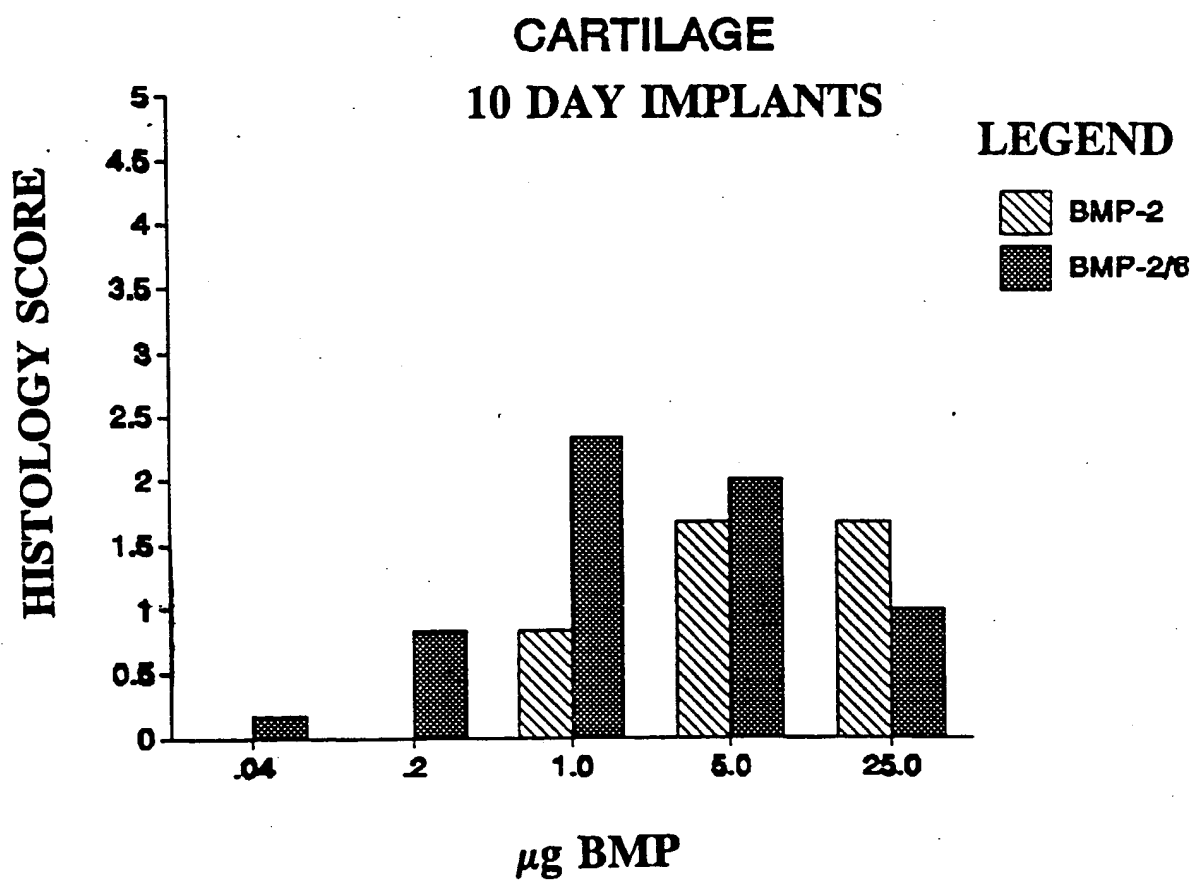
W-20 ALKALINE PHOSPHATASE: CHO BMP-2/6 vs. CHO BMP-2



SUBSTITUTE SHEET

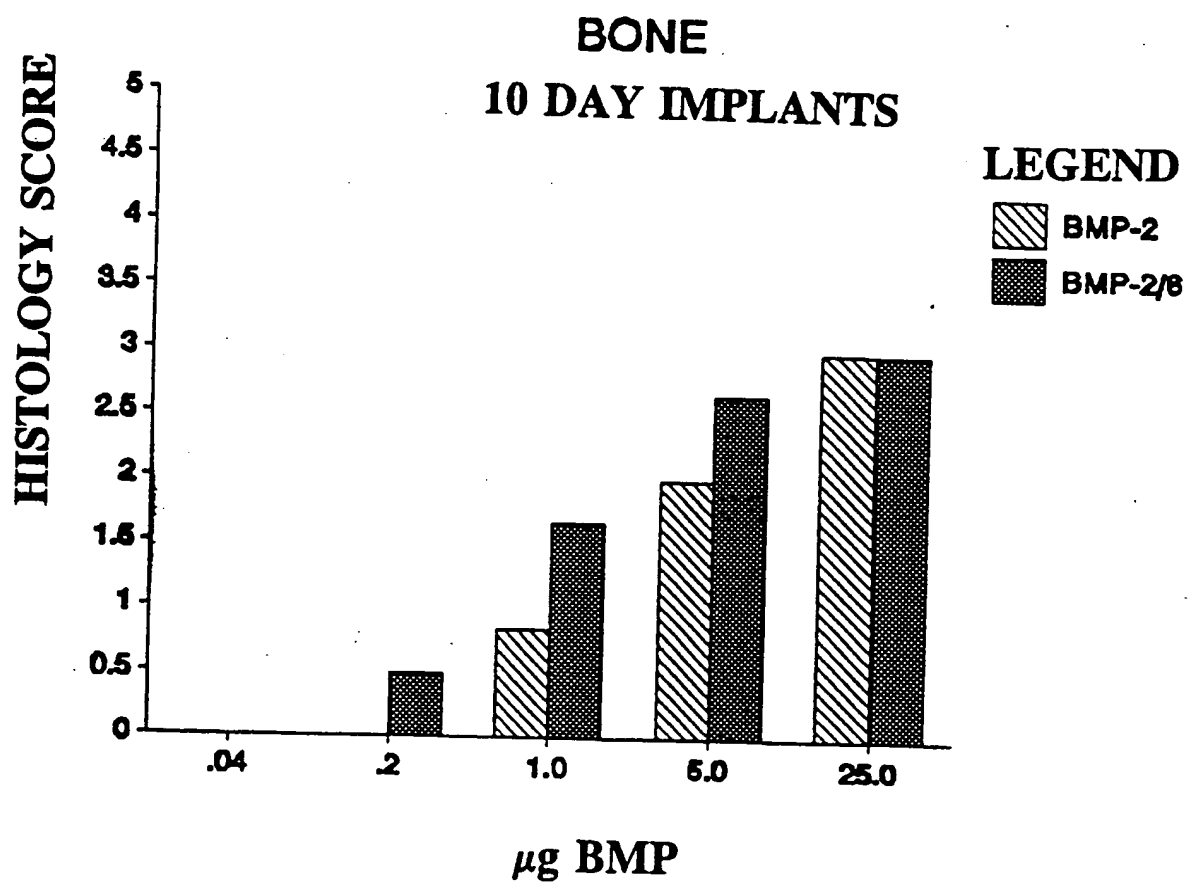
29/32

FIGURE 13A



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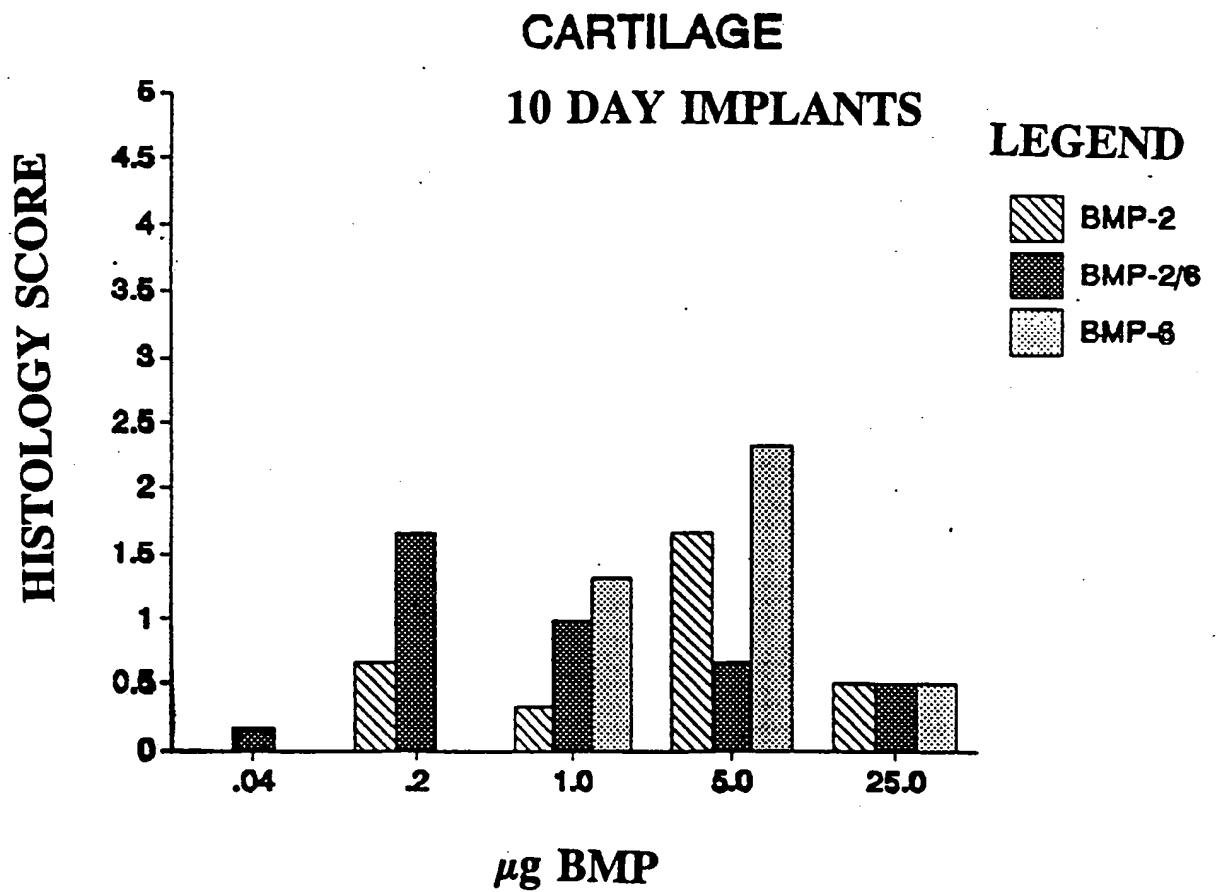
30/32

FIGURE 13B

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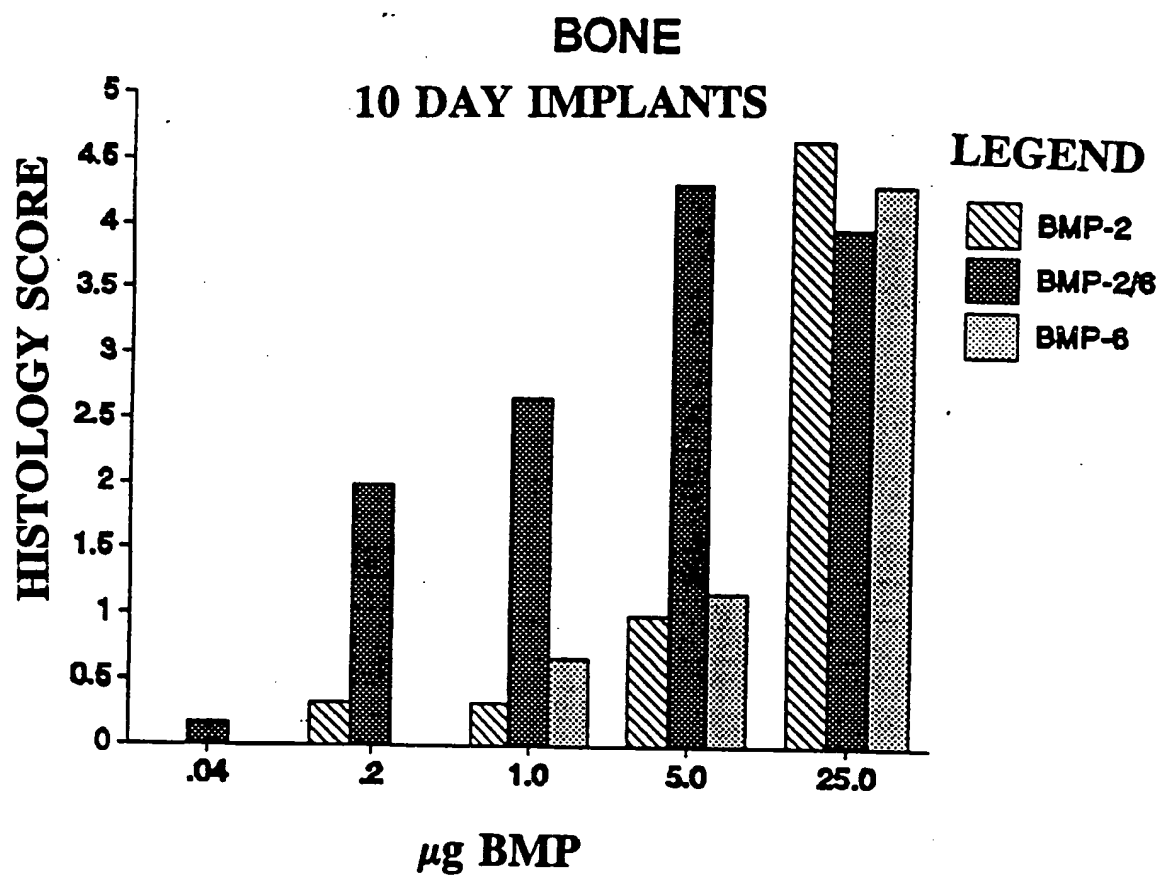
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FIGURE 14A



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FIGURE 14B

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 92/09430

I. CLASSIFICATION OF SUBJECT MATTER (If several classification symbols apply, indicate all) ⁶		
According to International Patent Classification (IPC) or to both National Classification and IPC		
Int.Cl. 5 C12N15/12; C12P21/02; A61K37/02; C12N5/12 C07K15/06		
II. FIELDS SEARCHED		
Minimum Documentation Searched ⁷		
Classification System	Classification Symbols	
Int.Cl. 5	C07K ; C12N ; A61K ; C12P	
Documentation Searched other than Minimum Documentation to the extent that such Documents are included in the Fields Searched ⁸		
III. DOCUMENTS CONSIDERED TO BE RELEVANT⁹		
Category ¹⁰	Citation of Document, ¹¹ with indication, where appropriate, of the relevant passages ¹²	Relevant to Claim No. ¹³
X	WO,A,9 003 733 (INTERNATIONAL GENETIC ENGINEERING, INC.) 19 April 1990 see page 16, line 7 - page 17, line 28 see page 18, line 22 - line 34	1,4, 7-14, 16, 23-26
Y	see page 51, line 32 - page 52, line 10; figure 12 see page 62 - page 63; claim 35 ---	13-17, 33,35
Y	WO,A,9 011 366 (GENETICS INSTITUTE, INC.) 4 October 1990 cited in the application see page 22, line 20 - line 27 see page 43, line 17 - line 30 ---	13-16,33
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<p>¹⁰ Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"A" document member of the same patent family</p>		
IV. CERTIFICATION		
Date of the Actual Completion of the International Search		Date of Mailing of this International Search Report
04 FEBRUARY 1993		26. 02. 93
International Searching Authority		Signature of Authorized Officer
EUROPEAN PATENT OFFICE		ANDRES S.M.

III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
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X	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA vol. 87, March 1990, WASHINGTON US pages 2220 - 2224 WANG, E.A. ET AL. 'Recombinant human bone morphogenetic protein induces bone formation' cited in the application see figure 1C ---	34,36
Y		35
X	JOURNAL OF BIOLOGICAL CHEMISTRY vol. 265, no. 22, 5 August 1990, BALTIMORE, MD US pages 13198 - 13205 SAMPATH, T.K. ET AL. 'Bovine osteogenic protein is composed of dimers of OP-1 and BMP-2A, two members of the transforming growth factor-beta superfamily' see the whole document ---	34,36
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A		13,16
A	WO,A,8 909 787 (CREATIVE BIOMOLECULES, INC.) 19 October 1989 see page 6, line 22 - line 24 see page 56, paragraphs E5 & E6 ---	
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III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)		
Category *	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
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ANNEX TO THE INTERNATIONAL SEARCH REPORT ON INTERNATIONAL PATENT APPLICATION NO.

US 9209430
SA 66918

This annex lists the patent family members relating to the patent documents cited in the above-mentioned international search report.
The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information. 04/02/93

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